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All search here

Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1 _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
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WWW/Internet: _____
Other (specify): _____

AT	CP	100	07
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HSSP/ Q14188; JCF/.

ID	ORGANISM	PRELIMINARY	PRG	290 AA.
AC	09C927			
AD	09C927			
DE	01-JUN-2001 (Tremblere, 17, Created)			
DT	01-JUN-2001 (Tremblere, 17, Last sequence update)			
DT	01-DEC-2001 (Tremblere, 19, Last annotation update)			
DE	TRANSCRIPTION FACTOR DP 1.			
GN	TFDP1.			
OC	Mus musculus (Mouse).			
OC	Eumetazoa: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
OC	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae			
OX	MCA1_Textid-100950:			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CE78L/63; TISSUE=EMBRYO:			
RC	MSDLINE=21063650: PubMed=11217631:			
RA	Kawai J., Shimogawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arizawa T., Hara A., Fukunishi Y., Kanno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamaneke I.,			
RA	Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Pletschmann N., Gaestelard T., Ghisla C., Kling B., Kochava H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nishida I., Pascoe O., Ooshimomura J.,			
RA	Schmitt L.M., Stabill P., Suzuki R., Tomita M., Wagner B., Mashio T.,			
RA	Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barth G.,			
RA	Blake J., Botfield D., Boyjunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Guinechevitch S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Nishina J., Mazzarelli J., Momberta P.,			
RA	Mordone P., Ring B., Ringwald C., Rodriguez I., Saito M.,			
RA	Sasaki H., Saito K., Schenckeborn C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Togo-Oka K., Wang K.H., Wette C., Whitaker C., Wilmink L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa T., Kaveaji H., Kontoukaki S.,			
RA	Hayashizaki Y.			
RT	Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
RL	EMBL: AK013180; BAB26595.1; --			
DR	HSSP: Q14188; ICP7.			

Page 2

DE TRANSCRIPTION FACTOR DP (FROGMENT).

GN DP OR C04654.
 OC Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pharyngota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC K011_TaxID=7227;
 (1)
 RP SEQUENCE FROM N.A.
 RA Koyman J., Whitaker A.J., Orr-Heaver T.L.,
 RA Genes Dev. 0:0-0(1997).
 DR EMBL: AF011363; AAA87765.1; ..
 DR HSP: Q14188; 1CF7.
 DR FLYbase: F89n0011763; DP.
 DR InterPro: IPR003116; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 DR MCL_TER 1 1
 FT SEQUENCE 363 AA; 4188 MW; 61DC66773BA43D42 CRC64;
 SO

Query Match 89.2% Score 166; DB 5; Length 363;
 Best Local Similarity 86.1%; Pred. No. 3e-15;
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Caps 0;
 Oy 1 KNIRRYDALVLMANNISREKKEIKWIGLPTNS 36
 DB 111 KNIRRYDALVLMANNISREKKEIKWIGLPTNS 156

RESULT 6
 09V6M0 PRELIMINARY; PRT: 445 AA.

AC 09V6M0; 017472;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE DP GENE PRODUCT (TRANSCRIPTION FACTOR E2F DP SUBUNIT).
 GN DP OR C04654.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pharyngota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 (1)
 RP SEQUENCE FROM N.A.
 RA Adams W.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga C., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.R., Chapple M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Abeyaratne A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Baller R.M., Banu A., Barendse J., Bayraktarov L., Basalyk E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
 RA Botova D., Botchan N.R., Bouck J., Brostman P., Brotherton P.,
 RA Butts R.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavan S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo J., Delcher A., Deng X., Meyers A.D., Dev T., Dietz S.W.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Duthin K.J., Evangelista C.C., Ferraz C., Fertizera S., Fleischmann W.,
 RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong P., Gottlieb J.H., Gu T., Guan P., Harris M.,
 RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
 RA Jaitell M., Kaulush P., Keipen G.H., Ke S., Kenson J.A., Ketchum K.A.,
 RA Kimmel A.E., Kodira C.D., Kraft C., Kravitz S., Rupp D., Lai Z.,
 RA Lako P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu K., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Minkov G., Minshtin N.V., Mobarry C., Morris J., Koshdel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy C., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Russkern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shie B.C., Siden-Kiamos I., Stappan M., Stupski M.P., Satch T.,
 RA Slater E., Spredling A.C., Stappan M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang L.-Y., Wasserman D.A., Weinlock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Yaver J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong P.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gbde R.A., Hyers E.W., Rubin G.M., Venter J.C.,
 RA The genome sequence of Drosophila melanogaster.
 RL Science 287:2185-2195(2000).
 (2)
 RP SEQUENCE OF 1-61 FROM N.A.
 RA MEDLINE:98078671; PubMed-9418862;
 RA Duronio R.J., Bonnette P.C., O'Farrell P.H.,
 RA Mutations of the Drosophila ddp, dezf, and cyclin E genes reveal
 RA distinct roles for the E2F-DP transcription factor and cyclin E during
 RA the G1-S transition.
 RL Mol. Cell Biol. 18:141-151(1998).
 DR EMBL: AF003819; MAF8403.1; ..
 DR EMBL: AF031700; MAF02971.1; ..
 DR HSP: Q14188; 1CF7.
 DR FLYbase: F89n0011763; DP.
 DR InterPro: IPR003116; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 DR MCL_TER 1 1
 FT SEQUENCE 445 AA; 49749 MW; 87F4DB826CE2E42 CRC64;
 SO

Query Match 89.2% Score 166; DB 5; Length 445;
 Best Local Similarity 86.1%; Pred. No. 3.7e-15;
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Caps 0;
 Oy 1 KNIRRYDALVLMANNISREKKEIKWIGLPTNS 36
 DB 213 KNIRRYDALVLMANNISREKKEIKWIGLPTNS 240

RESULT 7

AC 09H254 PRELIMINARY; PRT: 233 AA.
 DT 01-OCT-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE E2F-LIKE PROTEIN.
 GN HCA651.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 (1)
 RP SEQUENCE FROM N.A.
 RA Tissue-Liver;
 RA Pang X., Vaughan H., Chen N., Stclair F., Han K., Gabon J.,
 RA Cloning and characterization of novel genes related to hepatocellular
 RA carcinoma.
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF219119; AAF73562.1; ..
 DR HSP: Q14188; 1CF7.
 DR InterPro: IPR003116; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 DR MCL_TER 233 AA; 26053 MW; C5F9F8D2B7364784 CRC64;
 SO

Query Match 88.2% Score 164; DB 4; Length 233;
 Best Local Similarity 86.5%; Pred. No. 3.6e-15;
 Matches 32; Conservative 3; Mismatches 2; Indels 0; Caps 0;

Oy 1 KNIRRYDALVLMANNISREKKEIKWIGLPTNSA 37
 DB 99 KNIRRYDALVLMANNISREKKEIKWIGLPTNSA 135

RESULT 8
 O9L55 PRELIMINARY: PRT: 385 AA.
 AC O9L55
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DP-LIKE PROTEIN.
 GN DPA.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20562805; PubMed-1110847;
 RA Mayar E., Atanaseva A., de Veylder L., Rombauts S., Inze D.;
 RT "Characterization of two distinct DP-related genes from Arabidopsis
 thaliana."
 RL FEBS Lett. 486:79-87(2000).
 DR EMBL: AJ294532; CAC15484.1;
 DR HSSP: Q14188; ICF7.
 DR InterPro: IPR003316; E2F-TDP.
 DR Pfam: PF02319; E2F-TDP; 1.
 SO SEQUENCE 385 AA; 41755 MW; 5DB4ACAD0C52AF8 CRC64;

Query Match 81.2%: Score 151; DB 10; Length 385;
 Best Local Similarity 83.3%; Pred. No. 4,1e-11;
 Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 KNIRRYDALNVLMNNISKEKIKVIGLPTMS 36
 DB 157 KNIRRYDALNVLMNNISKEKIKVIGLPTMS 187

RESULT 9
 O9L57 PRELIMINARY: PRT: 413 AA.
 AC O9L57
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE TRANSCRIPTION FACTOR-LIKE PROTEIN.
 GN P1384_160.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Bevan M., Pohl T., Weisenegger T., Bancroft I., Meyers H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162751; CAB81399.1;
 DR HSSP: Q14188; ICF7.
 DR InterPro: IPR003316; E2F-TDP.
 DR Pfam: PF02319; E2F-TDP; 1.
 SO SEQUENCE 413 AA; 45604 MW; 239DC6DAED2F723 CRC64;

Query Match 81.2%: Score 151; DB 10; Length 413;
 Best Local Similarity 83.3%; Pred. No. 4,5e-11;
 Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 KNIRRYDALNVLMNNISKEKIKVIGLPTMS 36
 DB 157 KNIRRYDALNVLMNNISKEKIKVIGLPTMS 187

DB 169 KNIRRYDALNVLMNNISKEKIKVIGLPTMS 204

RESULT 10
 O9L55 PRELIMINARY: PRT: 288 AA.
 AC O9L55
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DP-2 TRANSCRIPTION FACTOR-LIKE.
 GN T22P11_60.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Bancroft I., Meyers H.W., Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162971; CAB85984.1;
 DR HSSP: Q14188; ICF7.
 DR InterPro: IPR003316; E2F-TDP.
 DR Pfam: PF02319; E2F-TDP; 1.
 SO SEQUENCE 288 AA; 32560 MW; ECAD07DC06E92B7 CRC64;

Query Match 73.1%: Score 136; DB 10; Length 288;
 Best Local Similarity 75.8%; Pred. No. 4e-11;
 Matches 25; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KNIRRYDALNVLMNNISKEKIKVIGLPTMS 33
 DB 99 KNIRRYDALNVLMNNISKEKIKVIGLPTMS 131

RESULT 11
 O9L53 PRELIMINARY: PRT: 292 AA.
 AC O9L53
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DP-LIKE PROTEIN (EC 6.3.2.19).
 GN DPA.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20562805; PubMed-1110847;
 RA Mayar E., Atanaseva A., de Veylder L., Rombauts S., Inze D.;
 RT "Characterization of two distinct DP-related genes from Arabidopsis
 thaliana."
 RL FEBS Lett. 486:79-87(2000).
 DR EMBL: AJ294531; CAC15483.1;
 DR HSSP: Q14188; ICF7.
 DR InterPro: IPR003316; E2F-TDP.
 DR Pfam: PF02319; E2F-TDP; 1.
 SO SEQUENCE 292 AA; 33038 MW; 644324E13561FEC5 CRC64;

Query Match 73.1%: Score 136; DB 10; Length 292;
 Best Local Similarity 75.8%; Pred. No. 4,1e-11;

Matches 25; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KNIRRYDALVLMANNISKEKKEINIGLP 33
 DB 103 KNIRRYDALVLMANNISKEKKEINIGLP 135

RESULT 12

ID 09871 PRELIMINARY; PRT: 261 AA.
 AC 09871;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE DP PROTEIN.
 GN DP.
 OS Triticum sp.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4559;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20562804; PubMed-1108846;
 RA Ramirez-Parra E., Gutierrez C.;
 RT "Characterization of wheat DP, a heterodimerization partner of the
 RT plant ZIP transcription factor which stimulates ZIP1 DNA binding."
 RL FEBS Lett. 486:73-78(2000)
 DR EMBL: AJ271917; CAC19034.1;
 DR HSSP: Q14188; ICF7.
 DR InterPro: IPR003316; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 SO SEQUENCE 261 AA; 29262 MW; 50088F193163A28 CRC64;

Query Match

Best Local Similarity 71.5%; Score 133; DB 10; Length 261;
 Matches 24; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KNIRRYDALVLMANNISKEKKEINIGLP 32
 DB 110 KNIRRYDALVLMANNISKEKKEINIGLP 141

RESULT 13

ID 09818 PRELIMINARY; PRT: 287 AA.
 AC 09818;
 DT 01-JUN-2001 (TRENBLREL. 17, Created)
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE EFL-2.
 GN EFL-2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-21394624; PubMed-11463372;
 RA Ceol C.J., Morville R.R.;
 RT Gp1-1 DP and e1-1, E2F Act with 1in-35 Rb to Antagonize Ras Signaling
 RT in C. elegans Vulval Development.
 RL Mol. Cell 7:461-473(2001).
 DR EMBL: AY028167; AA019033.1;
 DR HSSP: Q16354; ICF7.
 DR InterPro: IPR003316; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 SO SEQUENCE 287 AA; 32373 MW; 434446B88EC7A8 CRC64;

Query Match 44.4%; Score 82.5; DB 5; Length 287;
 Best Local Similarity 50.0%; Pred. No. 0.0014;

Matches 17; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

OY 4 KRRYDALVLMANNISKEKKEINIGLP 36
 DB 74 KRRYDALVLMANNISKEKKEINIGLP 107

RESULT 14

ID 090289 PRELIMINARY; PRT: 412 AA.
 AC 090289;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
 DE Y48C3A.17 PROTEIN.
 GN Y48C3A.17.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wallis J.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99069613; PubMed-9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology."
 RL Science 283:2012-2016(1998)
 DR EMBL: AL11203; CAB60421.1;
 DR HSSP: Q16254; ICF7.
 DR InterPro: IPR003316; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 SO SEQUENCE 412 AA; 45947 MW; 8F89D8280D54371 CRC64;

Query Match

Best Local Similarity 44.4%; Score 82.5; DB 5; Length 412;
 Matches 17; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

OY 4 KRRYDALVLMANNISKEKKEINIGLP 36
 DB 71 KRRYDALVLMANNISKEKKEINIGLP 104

RESULT 15

ID 095K01 PRELIMINARY; PRT: 281 AA.
 AC 095K01;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE RHOXHECTICAL 31.7 KDa PROTEIN.
 OS Macaca fascicularis (Cycad eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-TEMPORAL LOBE RIGHT;
 RA Otsuda M., Hida M., Kusuda J., Tanuma R., Iseki K., Hiral M., Teruo K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB060895; BAB46898.1;
 DR Hypothetical protein.
 SO SEQUENCE 281 AA; 31732 MW; FD1A9F7C2EE0D5 CRC64;

us-09-900-147-1.rpt

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Search completed: August 28, 2002, 13:03:00
Job time: 221 sec

Wed Aug 28 13:32:30 2002

us-09-900-147-1.rpx

Page 1

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OM protein - protein search, using sv model

Run on: August 28, 2002, 12:57:49 ; Search time 18.36 seconds

(without alignments)
193,644 Million cell updates/sec

Title: US-09-900-147-1

Perfect score: 186

Sequence: 1 KNIRRVYDALVLYAMNHSKEKKEIKVIGLPTNSA 37

Scoring table: BLOSUM62

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	410	2	transcription fact
2	186	100.0	410	2	transcription fact
3	186	100.0	410	2	transcription fact
4	186	100.0	410	2	transcription fact
5	186	100.0	410	2	transcription fact
6	186	100.0	410	2	transcription fact
7	186	100.0	410	2	transcription fact
8	186	100.0	410	2	transcription fact
9	186	100.0	410	2	transcription fact
10	186	100.0	410	2	transcription fact
11	186	100.0	410	2	transcription fact
12	186	100.0	410	2	transcription fact
13	186	100.0	410	2	transcription fact
14	186	100.0	410	2	transcription fact
15	186	100.0	410	2	transcription fact
16	186	100.0	410	2	transcription fact
17	186	100.0	410	2	transcription fact
18	186	100.0	410	2	transcription fact
19	186	100.0	410	2	transcription fact
20	186	100.0	410	2	transcription fact
21	186	100.0	410	2	transcription fact
22	186	100.0	410	2	transcription fact
23	186	100.0	410	2	transcription fact
24	186	100.0	410	2	transcription fact
25	186	100.0	410	2	transcription fact
26	186	100.0	410	2	transcription fact
27	186	100.0	410	2	transcription fact
28	186	100.0	410	2	transcription fact
29	186	100.0	410	2	transcription fact

30	53	28.5	334	2	glycolate oxidase
31	53	28.5	610	2	hypothetical prote
32	52.5	28.2	292	2	uncharacterized st
33	52	28.0	369	2	O-antigen translat
34	52	28.0	388	2	hypothetical prote
35	52	28.0	967	2	hypothetical prote
36	51.5	27.7	901	2	transcription elon
37	51	27.4	307	2	6-phosphofructokin
38	51	27.4	395	2	acetate kinase (EC
39	51	27.4	1829	2	hypothetical prote
40	50.5	27.2	240	2	RNA polymerase sig
41	50.5	27.2	282	2	hypothetical prote
42	50.5	27.2	419	2	hypothetical prote
43	50	26.9	185	2	hypothetical prote
44	50	26.9	456	2	iron-regulated ABC
45	50	26.9	600	2	probable ATP-depen

ALIGNMENTS

RESULT 1
B48585
transcription factor DRP1 chain 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Nov-1994 (sequence, revision 11-Nov-1994 text_change 10-Dec-1993)
C:Accession: B48585; S38372; S38371
R:Hein, K.; Wu, C.L.; Fellecy, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C.; Harlow
Gene Dev. 7, 1850-1861, 1993
A:Title: Heterodimerization of the transcription factors E2F-1 and DP-1 leads to c
A:Reference number: A48585; MUID:94010284
A:Accession: B48585
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-410 <HEL>
R:Girling, R.
submitted to the EMBL Data Library, July 1993
A:Reference number: S38372
A:Accession: S38372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-410 <GIR>
A:Cross-references: EMBL:72310; MID:9395280; PDB:CAA51056.1; PID:9395281
R:Girling, R.; Partridge, J.F.; Bandara, L.R.; Burden, N.; Totty, M.F.; Heuvel, J.J
Nucleic Acids Res. 21, 1681-1688, 1993
A:Title: A new component of the transcription factor DRP1/E2F.
A:Reference number: S38371; MUID:94019777
A:Accession: S38371
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 188-410 <G12>
A:Cross-references: EMBL:72310
C:Superfamily: transcription factor DP
C:Keywords: DNA binding; transcription factor

Query Match 100.0% Score 186; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 5.3e-18;
Matches 37; Conservative 0; Mismatches 0; Indels 0;

DB 163 KNIRRVYDALVLYAMNHSKEKKEIKVIGLPTNSA 37
1 KNIRRVYDALVLYAMNHSKEKKEIKVIGLPTNSA 199

RESULT 2
A48585
transcription factor DRP-1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Nov-1994 (sequence, revision 11-Nov-1994 text_change 10-Dec-1993)
C:Accession: A48585
R:Hein, K.; Wu, C.L.; Fellecy, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C.; Harlow
Gene Dev. 7, 1850-1861, 1993

A:Title: Heterodimerization of the transcription factors E2F-1 and DP-1 leads to cooperat

A:Reference number: M8385; MID:94010284

A:Accession: A48585

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-410 <BEL>

A:Cross-references: GB:L23959; MID:9441316; PIDM:AA58440.1; PID:9413317

C:Superfamily: transcription factor DP

C:Keywords: DNA binding; transcription factor

Query Match 100.0%; Score 186; DB 2; Length 410;

Best Local Similarity 100.0%; Pred. No. 5,3e-18;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 37

DB 163 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 159

RESULT 3

hypothetical protein DKF2P43G22.1 - human (fragment)

A:Alternate names: E2F dimerization partner 2

C:Species: Homo sapiens (man)

C:Date: 23-Jul-1999 sequence, revision 23-Jul-1999 text, change 17-Nov-2000

C:Accession: T12511; A57381; I37297; I39180

R:Amberg, M.; Mitter, U.; Meyer, H.W.; Gassenhuber, J.; Wilmann, S.

submitted to the Protein Sequence Database, June 1999

A:Reference number: 217527

A:Accession: T12511

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 <ANS>

A:Cross-references: EMBL:AL080206

A:Experimental source: adult testis; clone DKF2P43G22

R:Mu, C.L.; Zuberberg, L.R.; Ngwu, C.; Harlow, E.; Lees, J.A.

Mol. Cell. Biol. 15, 2536-2546, 1995

A:Title: In vivo association of E2F and DP family proteins.

A:Reference number: A57381; MID:9557935

A:Accession: A57381

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 <ANS>

A:Cross-references: GB:L40386; MID:9703084; PIDM:AA69016.1; PID:9703085

R:Zheng, Y.; Chellappan, S.P.

Oncogene 10, 2085-2093, 1995

A:Title: Cloning and characterization of human DP2, a novel dimerization partner of E2F

A:Reference number: I37297; MID:95103470

A:Accession: I37297

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-33-143, 144-416 <ZHA>

A:Cross-references: EMBL:U018422; MID:9604478; PIDM:AA660378.1; PID:9604479

A:Accession: I39180

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-33-49 <ZHA>

A:Cross-references: EMBL:U03117; MID:91008545; PIDM:AA60642.1; PID:91008546

C:Genetics:

A:Gene: GDB:TFDP2; DP2

A:Cross-references: GDB:638814

A:Map position: 12323-12323

A:Note: DKF2P43G22.1

C:Superfamily: transcription factor DP

Query Match 100.0%; Score 186; DB 2; Length 416;

Best Local Similarity 100.0%; Pred. No. 5,4e-18;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 37

DB 163 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 159

RESULT 3

hypothetical protein DKF2P43G22.1 - human (fragment)

A:Alternate names: E2F dimerization partner 2

C:Species: Homo sapiens (man)

C:Date: 23-Jul-1999 sequence, revision 23-Jul-1999 text, change 17-Nov-2000

C:Accession: T12511; A57381; I37297; I39180

R:Amberg, M.; Mitter, U.; Meyer, H.W.; Gassenhuber, J.; Wilmann, S.

submitted to the Protein Sequence Database, June 1999

A:Reference number: 217527

A:Accession: T12511

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 <ANS>

A:Cross-references: EMBL:AL080206

A:Experimental source: adult testis; clone DKF2P43G22

R:Mu, C.L.; Zuberberg, L.R.; Ngwu, C.; Harlow, E.; Lees, J.A.

Mol. Cell. Biol. 15, 2536-2546, 1995

A:Title: In vivo association of E2F and DP family proteins.

A:Reference number: A57381; MID:9557935

A:Accession: A57381

DB 148 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 184

RESULT 4

transcription factor DRF1 chain 1 - mouse

A:Accession: S30049

A:Alternate names: transcription factor DP-1

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 sequence, revision 10-Sep-1993 text, change 10-Dec-1999

C:Accession: S30049; S34572

R:Girling, R.; Partidge, J.F.; Bandaru, L.R.; Burden, N.; Totty, N.F.; Hansen, J.J.

Nature 362, 83-87, 1993

A:Title: A new component of the transcription factor DRF1/E2F.

A:Reference number: S30049; MID:93188967

A:Accession: S30049

A:Molecule type: mRNA

A:Residues: 1-429 <GTR>

A:Cross-references: EMBL:X72310

A:Accession: S34572

A:Molecule type: protein

A:Residues: 75-90; 131-151; 164-184; 191-207; 215-249; 261-293; 302-313; 321-328 <GTR>

C:Superfamily: transcription factor DP

C:Keywords: DNA binding; transcription factor

P184-204/Domain: DNA binding status predicted <DNA>

Query Match 100.0%; Score 186; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 5,6e-18;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 37

DB 163 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 199

RESULT 3

transcription factor DP - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 25-Aug-1995 sequence, revision 25-Aug-1995 text, change 10-Dec-1999

C:Accession: B55745

R:Dynlacht, B.D.; Brock, A.; Dembak, M.; Yennah, L.; Dyson, N.

Proc. Natl. Acad. Sci. U.S.A. 91, 6359-6363, 1994

A:Title: DNA-binding and trans-activation properties of Drosophila E2F and DP prote

A:Reference number: A55745; MID:94294181

A:Accession: B55745

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-377 <DYN>

A:Cross-references: GB:X79708; MID:9516866; PID:9516867

C:Genetics:

A:Gene: FlyBase:DP

A:Cross-references: FlyBase:FBgn0011763

C:Superfamily: transcription factor DP

Query Match 89.3%; Score 166; DB 2; Length 377;

Best Local Similarity 86.1%; Pred. No. 2,9e-15;

Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 36

DB 145 KNIRRVYDALVLMANNISKEKIKWGLPTNSA 180

RESULT 6

hypothetical protein T2367.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 sequence, revision 15-Oct-1999 text, change 15-Oct-1999

C:Accession: T23207

R:Barlow, K.

submitted to the EMBL Data Library, December 1995

A:Reference number: 219995

A:Accession: T23207

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-598 <NTL>

A:Cross-references: EMBL:268319; PIDN:CAA92699.1; GSPDB:GMO0020; CESP:72367.1

A:Experimental source: clone T2367

C:Genetics:

A:Gene: CESP:72367.1

A:Map position: 2

A:Introns: 3/21 115/3; 204/21 227/2; 260/1; 298/1; 363/1; 424/3; 478/3; 565/1

Query Match

Best Local Similarity 82.3%; Score 153; DB 2; Length 598;

Best Local Similarity 75.7%; Pred. No. 3.2e-13;

Matches 28; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 122 KIRRRYDALNVLMMNITSEKREINWIGLPTNSA 37

1 KIRRRYDALNVLMMNITSEKREINWIGLPTNSA 37

122 KIRRRYDALNVLMMNITSEKREINWIGLPTNSA 158

RESULT 7

transcription factor-like protein - Arabidopsis thaliana

N:Alternate names: protein P12E4.160

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 (sequence_revision 20-Apr-2000 (text_change 20-Apr-2000

C:Accession: T48364

R:Byron, M.; Pohl, T.; Wellenreger, T.; Bancroft, I.; Mewes, H.N.; Rudd, S.; Lemcke, K.;

submitted to the Protein Sequence Database, March 2000

A:Reference number: 22493

A:Accession: T48364

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-413 <BEV>

A:Cross-references: EMBL:AL162751

A:Experimental source: cultivar Columbia; BAC clone P12E4

C:Genetics:

A:Map position: 5

A:Introns: 84/2; 128/1; 163/3; 212/3; 249/1; 279/3; 303/2

A:Note: P12E4.160

Query Match

Best Local Similarity 81.2%; Score 151; DB 2; Length 413;

Best Local Similarity 83.3%; Pred. No. 4e-13; 3; Indels 0; Gaps 0;

Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 1 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 36

169 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 204

RESULT 8

transcription factor-like - Arabidopsis thaliana

N:Alternate names: protein T22P11.60

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 (sequence_revision 20-Apr-2000 (text_change 20-Apr-2000

C:Accession: T48268

R:Byron, M.; Milbert, M.; Braun, M.; Holzer, B.; Brandt, A.; Duesterhoft, A.; Bancroft,

submitted to the Protein Sequence Database, April 2000

A:Reference number: 22490

A:Accession: T48268

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <BEV>

A:Cross-references: EMBL:AL162971

A:Experimental source: cultivar Columbia; BAC clone T22P11

C:Genetics:

A:Map position: 5

A:Introns: 36/2; 57/1; 71/2; 95/3; 142/3; 163/3; 198/3; 222/2

A:Note: T22P11.60

Query Match

Best Local Similarity 73.1%; Score 136; DB 2; Length 288;

Best Local Similarity 75.8%; Pred. No. 3.3e-11;

Matches 25; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 1 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 32

99 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 131

RESULT 9

hypothetical protein Y48C3A.c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 (sequence_revision 29-Oct-1999 (text_change 29-Oct-1999

C:Accession: T31602

R:Wallis, J.

submitted to the EMBL Data Library, September 1999

A:Reference number: 221046

A:Accession: T31602

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-470 <NTL>

A:Cross-references: EMBL:AL117203; NID:01549827; PIDN:CA85117.1; CESP:Y48C3A.c

A:Experimental source: clone Y48C3A

C:Genetics:

A:Gene: CESP:Y48C3A.c

A:Introns: 52/3; 156/2; 206/2; 237/3; 332/1; 386/1

Query Match

Best Local Similarity 44.4%; Score 82.5; DB 2; Length 470;

Best Local Similarity 50.0%; Pred. No. 0.0016;

Matches 17; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

Db 4 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 36

129 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 162

RESULT 10

T31005

hypothetical protein T24C30.40 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 13-Aug-1999 (sequence_revision 13-Aug-1999 (text_change 22-Oct-1999

C:Accession: T13005

R:Choi, N.; Robert, C.; Brothier, P.; Wincker, P.; Carrotto, L.; Artiguenave,

submitted to the Protein Sequence Database, July 1999

A:Reference number: 217586

A:Accession: T13005

A:Molecule type: DNA

A:Residues: 1-323 <CHD>

A:Cross-references: EMBL:AL096856; GSPDB:GMO0061; ATSP:T27320.40

A:Experimental source: cultivar Columbia; BAC clone T24C30

C:Genetics:

A:Map position: 3

A:Introns: 12/1; 29/3; 55/3; 73/3; 111/1; 133/3; 159/1; 179/3

Query Match

Best Local Similarity 38.7%; Score 72; DB 2; Length 323;

Best Local Similarity 45.5%; Pred. No. 0.03;

Matches 15; Conservative 4; Mismatches 8; Indels 6; Gaps 1;

Db 5 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 31

162 KIRRRYDALNVLMMNITSEKREINWIGLPTNS 194

RESULT 11

transcription factor E2F1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 28-Apr-1995 sequence_revision 28-Apr-1995 text_change 05-Nov-1999
 C:Accession: A56209
 R.L.L. Y.: Slansky, J.E.; Meyer, D.J.; Drinkwater, M.R.; Keelin, W.G.; Farham, P.J.
 Mol. Cell. Biol. 14, 1861-1865, 1994
 A>Title: Cloning, chromosomal location, and characterization of mouse E2F1.
 A:Reference number: A56209; MIMD:94158658
 A:Accession: A56209
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-430 <L1>
 A:Cross-references: GB:121973; MIMD:91091479; PIMD:AA83217.1; PTD:9405524

Query Match 38.4%; Score 71.5; DB 2; Length 430;
 Best local similarity 43.8%; Pred. No. 0.049; 9; Indels 1; Gaps 1;
 Matches 14; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

OY 4 RRRVDAALVLMANNISKE-KKEIKWIGLPT 34
 DB 159 KRRIIDINVLGGIQLTKSKNNHIMWIGSHT 190

RESULT 12
 JCI4929
 transcription factor E2F1 - human
 N:Alternate names: A012 protein; retinoblastoma-associated protein; retinoblastoma-bind
 C:Species: Homo sapiens (man)
 C>Date: 22-Oct-1996 sequence_revision 01-Nov-1996 text_change 02-Jun-2000
 C:Accession: JCI4929; A45032; A42997; A44091
 R.Neuman, E.; Sellers, W.R.; McNeil, J.A.; Lawrence, J.B.; Keelin Jr., W.G.
 Gene 173, 163-169, 1996
 A>Title: Structure and partial genomic sequence of the human E2F1 gene.
 A:Reference number: JCI4929; MIMD:97082361
 A:Accession: JCI4929
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-437 <NR>
 A:Cross-references: GB:047675; MIMD:91594281; GB:047676; MIMD:91594282; GB:047677; MIMD:915
 A:Experimental source: placenta
 R.Shen, B.; Zhu, X.; Chen, P.L.; Durrfee, T.; Yang, Y.; Sharp, D.; Lee, W.H.
 Mol. Cell. Biol. 12, 5620-5631, 1992
 A>Title: Molecular cloning of cellular genes encoding retinoblastoma-associated proteins
 A:Reference number: A45032; MIMD:93078763
 A:Accession: A45032
 A:Molecule type: mRNA
 A:Residues: 1-437 <NR>
 A:Cross-references: GB:949992; MIMD:9266573; PIMD:AA82489.1; PTD:9260574
 A:Note: sequence extracted from NCBI Backbone (NCBI:119095)
 A:Note: the authors are uncertain whether Met-1 is the initiator or whether translation
 R.Hellin, R.; Lees, J.A.; Vidal, M.; Dyson, N.; Harlow, E.; Pattney, A.
 Cell 70, 337-350, 1992
 A>Title: A cDNA encoding a pRB-binding protein with properties of the transcription fact
 A:Reference number: A42998; MIMD:93346720
 A:Accession: A42998
 A:Molecule type: mRNA
 A:Residues: 1-312, 'S', 314-321, 'N', 323-328, 'T', 330-437 <NR>
 A:Cross-references: GB:945677; MIMD:9181917; PIMD:AA33782.1; PTD:9181918
 A:Experimental source: Nalm 6 pre-B leukemia cell line
 A:Note: sequence extracted from NCBI Backbone (NCBI:110035, NCBI:110016)
 R.Kiehl, J.F.; W.G.; Kiehl, W.; Sellers, W.R.; Decaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.
 Cell 70, 351-366, 1992
 A>Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F
 A:Reference number: A42997; MIMD:93346721
 A:Accession: A42997
 A:Molecule type: mRNA
 A:Residues: 1-312, 'S', 314-321, 'N', 323-328, 'T', 330-437 <NR>
 A:Cross-references: GB:010511; MIMD:9539713
 A:Experimental source: Amax cells; expression vector pGEX-2TK
 R.Johnson, D.G.; Ohtani, K.; Nevins, J.R.
 Genes Dev. 8, 1514-1525, 1994
 A>Title: Autoregulatory control of E2F1 expression in response to positive and negative
 A:Reference number: JCI4931; MIMD:95047311

A:Accession: 154091
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-68, 'R', 'T', 122-123, 'T', 127, 'G', 297-299, 'P', 308-309, 'A', 312, 'C'
 A:Cross-references: GB:574230; MIMD:9712816; PIMD:AA014150.1; PTD:94261850
 C:Genetics:
 A:Gene: GDB: 82F1
 A:Cross-references: GDB:134661; OMIM:189971
 A:Map position: 20q11-20q11
 A:Intons: 87/3 118/1 191/2 242/2 280/3 356/1
 C:Keywords: DNA binding; transcription factor
 F:67-108/Region: cyclin box status predicted
 F:118-190/Region: DNA binding status predicted <DN>
 F:131-211/Region: 7-residue repeats

Query Match 38.4%; Score 71.5; DB 2; Length 437;
 Best local similarity 43.8%; Pred. No. 0.05;
 Matches 14; Conservative 8; Mismatches 9; Indels 1; Gaps 1;
 OY 4 RRRVDAALVLMANNISKE-KKEIKWIGLPT 34
 DB 164 KRRIIDINVLGGIQLTKSKNNHIMWIGSHT 195

RESULT 13
 558345
 E2F-1 transcription factor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 11-Jan-1996 sequence_revision 01-Mar-1996 text_change 10-Sep-1997
 C:Accession: 558345
 R.Pastan, S.; Lohse, L.; Arnaud, L.; Trembleau, A.; Brun, G.
 submitted to the EMBL Data Library, June 1995
 A:Description: Isolation and characterization of a chicken homolog of the E2F-1 tra
 A:Reference number: 558345
 A:Accession: 558345
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-403 <PMS>
 A:Cross-references: EMBL:X89245; MIMD:944827; PTD:944828

Query Match 37.9%; Score 70.5; DB 2; Length 403;
 Best local similarity 44.8%; Pred. No. 0.053;
 Matches 13; Conservative 8; Mismatches 7; Indels 1; Gaps 1;
 OY 4 RRRVDAALVLMANNISKE-KKEIKWIG 31
 DB 141 KRRIIDINVLGGIQLTKSKNNHIMWIG 169

RESULT 14
 A54595
 transcription factor E2F-2 - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 sequence_revision 13-Jan-1995 text_change 08-Oct-1999
 C:Accession: A54595
 R.Riley-Hoyte, M.; Conroy, R.; Huber, M.E.; Goodheart, P.J.; Olf, A.; Helmbrook, D.
 Mol. Cell. Biol. 13, 7802-7812, 1993
 A>Title: Cloning and characterization of E2F-2, a novel protein with the biochemica
 A:Reference number: A54595; MIMD:94067141
 A:Accession: A54595
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-437 <YEC>
 A:Cross-references: GB:122846; MIMD:9410206; PIMD:AA16890.1; PTD:9410207
 C:Genetics:
 A:Gene: GDB: E2F2; E2F-2
 A:Cross-references: GDB: 270248; OMIM:600426
 A:Map position: 1p36-1p36
 C:Keywords: transcription factor

Query Match 37.4%; Score 69.5; DB 2; Length 437;
 Best Local Similarity 44.8%; Pred. No. 0.095;
 Matches 13; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
 QY 4 RRRVYDALVYLVANNISKE-KKEIKWIG 31
 :||:| ||| :||:| ||:|
 DB 166 KRRITDITWLEGIOLIRKAKNNIOWG 194

RESULT 19

AS6199
 Description factor E2F-1 - fruit fly (Drosophila melanogaster)
 Species: Drosophila melanogaster
 Date: 28-Apr-1995 sequence_revision 28-Apr-1995 text_change 21-Jul-2000
 Accession: AS6199; AS5745
 Olcanil, K.; Nevins, J.R.
 Mol. Cell. Biol. 14, 1603-1612, 1994
 Title: Functional properties of a Drosophila homolog of the E2F1 gene.
 Reference number: AS6199; MID:9415883
 Accession: AS6199
 Status: Preliminary
 Molecule type: mRNA
 Residues: 1-805 <ORF>
 Cross-references: GB:U10184; MID:9499103; PIDN:AA19003.1; PID:9499104
 Dynlacht, B.D.; Brook, A.; Dembki, M.; Yenush, L.; Dyson, N.
 Proc. Natl. Acad. Sci. U.S.A. 91, 6359-6363, 1994
 Title: DNA-binding and trans-activation properties of Drosophila E2F and DP proteins.
 Reference number: AS5745; MID:94294381
 Accession: AS5745
 Status: Preliminary; nucleic acid sequence not shown
 Molecule type: mRNA
 Residues: 1-805 <ORF>
 Cross-references: GB:X78421; MID:9516868; PIDN:CAA55186.1; PID:9516869
 Genetics:
 Gene: FlyBase:E2F1
 Cross-references: FlyBase:FBgn0011767

Query Match 36.3%; Score 67.5; DB 2; Length 805;
 Best Local Similarity 48.1%; Pred. No. 0.36;
 Matches 13; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
 QY 4 RRRVYDALVYLVANNISKE-KKEIKW 29
 :||:| ||| :||:| ||:|
 DB 291 KRRITDITWLEGIOLIRKAKNNIOW 317

Search completed: August 28, 2002, 12:59:59
 Job time: 130 sec

Wed Aug 28 13:32:29 2002

us-09-900-147-1.rag

Page 1

GenCore version 4.5
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ON protein - protein search, using sw model

Run on: August 28, 2002, 12:55:14 ; Search time 29.9 Seconds

(without alignments)
137,449 Million cell updates/sec

Title: US-09-900-147-1

Sequence: 1 ENIRRRYDALNVLNMTISKEKEIKWIGLPTNSA 37

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database:

1: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1980.DAT:
2: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1981.DAT:
3: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1982.DAT:
4: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1983.DAT:
5: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1984.DAT:
6: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1985.DAT:
7: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1986.DAT:
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9: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1988.DAT:
10: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1989.DAT:
11: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1990.DAT:
12: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1991.DAT:
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19: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1998.DAT:
20: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA1999.DAT:
21: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA2000.DAT:
22: /SIDSI/gcgdata/hold-geneeq/geneeq-emb1/AA2001.DAT:

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	37	19	AAW0501
2	186	100.0	149	22	ABG0510
3	186	100.0	333	22	NA674072
4	186	100.0	410	15	AA854653
5	186	100.0	410	17	AA889212
6	186	100.0	424	22	ABG28057
7	182	97.9	446	20	AA18025
8	162	89.2	445	22	ABG0852
9	162	87.1	183	22	ABG03508
10	158	84.9	119	21	AA83108
11	153	82.3	120	21	AA831007

12	153	82.3	575	20	AAW83389
13	152	81.7	30	19	AAW0507
14	151	81.2	277	21	AA62852
15	151	81.2	299	21	AA607975
16	151	81.2	344	21	AA62851
17	151	81.2	385	21	AA62850
18	144	77.4	194	20	AA123164
19	135	73.1	138	20	AA123161
20	133	71.5	56	22	AA67266
21	133	71.5	261	22	AA67262
22	116	62.4	83	20	AA13243
23	101	54.3	20	19	AAW0505
24	101	54.3	28	19	AAW0501
25	101	54.3	28	19	AAW0505
26	91	48.9	19	19	AAW0504
27	83	44.6	19	19	AAW0505
28	80	43.0	15	19	AAW0510
29	79	42.5	19	19	AAW0517
30	77	41.4	19	19	AAW0516
31	76	40.9	16	19	AAW0506
32	74.5	40.1	272	18	AAW2447
33	72.5	39.0	281	18	AAW3749
34	72.5	39.0	281	20	AA108415
35	72.5	39.0	15	19	AAW07052
36	71.5	38.7	15	19	AAW07052
37	71.5	38.4	437	14	AAW42458
38	71.5	38.4	437	19	AAW42458
39	71.5	38.4	437	19	AAW48389
40	71.5	38.4	437	20	AAW3913
41	71.5	38.4	437	21	AAW91046
42	71.5	38.4	476	15	AAW89287
43	69.5	37.4	437	16	AAW3234
44	69	37.1	14	19	AAW05211
45	68.5	36.8	465	22	ABG01736

ALIGNMENTS

RESULT 1
ID AAW0501 standard; Peptide: 37 AA.
XX
MC AAW0501:
XX
DT 26-OCT-1998 (first entry)
XX
DE DP-1 transcription factor peptide H (DEP box).
XX
XX DP-1 transcription factor; antagonist; E2F protein; apoptosis;
KW cell proliferation; cardiovascular cell; restenosis; tumour;
RW surgical stent; therapy.
XX
XX Synthetic.
OS Homo sapiens.
XX
PM W0928334-A1.
XX
PD 02-JUL-1998.
XX
PP 22-DEC-1997; 97WO-GB03506.
XX
PR 20-DEC-1996; 96GB-0026589.
XX
XX (PROL-) PROLIFIX LTD.
XX
XX Bandera LR, La Thangue NB;
XX WPI: 1998-377596/32.
XX
XX Polypeptide fragments of the DP-1 transcription factor - used for
PT inducing apoptosis, specifically in tumour and cardiovascular cells,
PT e.g. for preventing restenosis

XX Claim 1: Page 44: 55pp: English.
 XX
 CC Peptide M (I) comprises residues 163-199, i.e. the DEP box region,
 CC of transcription factor Dp1. Claimed fragments (II) (see AM20502-07)
 CC of (I) are capable of antagonizing the heterodimerisation of a DP
 CC protein with an E2F protein. Also claimed are fusion proteins
 CC (III) comprising (I) or (II) and a membrane translocation sequence
 CC (see AM20508), expression vectors encoding (I)-(III) and host cells
 CC (I)-(III) are used therapeutically to induce apoptosis,
 CC specifically in tumour or cardiovascular cells, either in vivo or in
 CC vitro, e.g. for purging bone marrow. Surgical stents comprising
 CC (I)-(III) are used to treat or prevent restenosis in patients who
 CC have undergone angioplasty. (I)-(III) function by inactivating
 CC the DNA-binding activity of DP/E2F heterodimers. They are also
 CC used as research reagents, as positive controls in assays for
 CC identifying antagonists of DP-1/E2F dimerisation and as immunos assay
 CC agents. Also described is the use of sequences antisense to
 CC nucleic acids encoding (I)-(III) to control DP levels in cells,
 CC particularly by gene therapy. When formulated with cytotoxic
 CC or cytostatic agents, (I)-(III) enhance cell killing.
 XX
 SQ Sequence 37 AA:

Query Match 100.0%; Score 186; DB 19; Length 37;
 Best Local Similarity 100.0%; Pred. No. 9, 8e-22;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KNTRRYDALVYAMNYSKEKKEKNGIPNSA 37
 ||||||||||||||||||||||||||||||||
 DB 1 KNTRRYDALVYAMNYSKEKKEKNGIPNSA 37

RESULT 2

ABG05510
 ID ABG05510 standard; Protein: 149 AA.

XX
 AC ABG05510;

XX
 DT 13-FEB-2002 (first entry)

XX
 DE Novel human diagnostic protein #5501.

XX
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX
 OS Homo sapiens.

XX
 PN WO200175067-A2.

XX
 PD 11-OCT-2001.

XX
 PE 30-MAR-2001; 2001WO-US08631.

XX
 PR 31-MAR-2000; 2000US-0540237.

XX
 PR 23-AUG-2000; 2000US-0619167.

XX
 PA (HUS-) HUSCO INC.

XX
 PI Dymac RT, Liu C, Tang YZ;

XX
 DR WPI: 2001-639362/73.

XX
 DR N-PSDB; AAS69697.

XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX
 PS Claim 20; SEQ ID NO 35869; 103pp: English.

XX
 CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantifying a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG0377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from HUSCO
 CC at ftp.vlpo.int/pub/publi/ahed_pcc_sequences.
 XX
 SQ Sequence 149 AA:

Query Match 100.0%; Score 186; DB 22; Length 149;
 Best Local Similarity 100.0%; Pred. No. 5, 3e-21;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KNTRRYDALVYAMNYSKEKKEKNGIPNSA 37
 ||||||||||||||||||||||||||||||||
 DB 22 KNTRRYDALVYAMNYSKEKKEKNGIPNSA 58

RESULT 3

AG74072
 ID AG74072 standard; Protein: 355 AA.

XX
 AC AG74072;

XX
 DT 03-SEP-2001 (first entry)

XX
 DE human colon cancer antigen protein SPO ID NO:4836.

XX
 KW Human: colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 13.

XX
 OS Homo sapiens.

XX
 PN WO200122920-A2.

XX
 PD 05-APR-2001.

XX
 PE 28-SEP-2000; 2000WO-US26534.

XX
 PR 29-SEP-1999; 98US-015407.

XX
 PR 03-NOV-1999; 93US-0163780..

XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX
 DR WPI: 2001-23537/74.

XX
 DR N-PSDB; AAG33503.

XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -

XX
 PS Claim 11; Page 6620-6621; 9803pp: English.

XX
 CC AAG32943 to AAG37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene

XX	PR	31-MAR-2000; 2000US-0540217.
XX	PR	23-AUG-2000; 2000US-0649167.
XX	PA	(HYSR-) HYSEQ INC.
XX	PI	Drmancac RT, Liu C, Tang YT;
XX	XX	WPI: 2001-639362/73.
DR	N-PSDB:	AAS656955.
DR	XX	
PT	PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	PT	diagnostics, forensics, gene mapping, identification of mutations
PT	PT	responsible for genetic disorders or other traits and to assess
PT	PT	biodiversity
XX	XX	
PS	claim 20;	seq ID NO 35867; 103pp; English.
CC	XX	The invention relates to isolated polynucleotide (I) and
CC	XX	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	XX	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	XX	and gene mapping, and in recombinant production of (II). The
CC	XX	polynucleotides are also used in diagnostics as expressed sequence tags
CC	XX	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	XX	to restore normal activity of (II) or to treat disease states involving
CC	XX	(II). (II) is useful for generating antibodies against it, detecting or
CC	XX	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	XX	a food supplement. (II) and its binding partners are useful in medical
CC	XX	treatment of sites expressing (II). (I) and (II) are useful for treating
CC	XX	disorders involving aberrant protein expression or biological activity.
CC	XX	The polypeptide and polynucleotide sequences have applications in
CC	XX	diagnostics, forensics, gene mapping, identification of mutations
CC	XX	and responsible for genetic disorders or other traits to assess biodiversity
CC	XX	and to produce other types of data and products dependent on DNA and
CC	XX	amino acid sequences. ABO00010-ABG10377 represent novel human
CC	XX	diagnostic amino acid sequences of the invention.
CC	XX	Note: The sequence data for this patent did not appear in the printed
CC	XX	specification, but was obtained in electronic format directly from WIPO
CC	XX	at ftp.wipo.int/pub/published_pct_sequences.
XX	sequence	185 AA:
QY	1 KAIRRRVDAALNTLANNMIRIKKRTKRWIGCLPNSA	37
DB	:::	
DB	149 KILTRIVCDGLNVLRAVALISKKKELKIGLPINSA	185
RESULT 10		
AAB3J108	ID	AAB3J108 standard; Protein: 119 AA.
XX	XX	
AC	AAB3J108;	
XX	XX	
DT	25-JAN-2001 (first entry)	
DE	Pinus radiata transcription factor protein sequence #235.	
KM	Plant: transcriptions factors; gene expression; eucalyptus; pine; acacia;	
KM	poplar; sweetgum; oak; mahogany; btiip; G-box binding factor;	
KM	basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;	
KM	homeodomain zipper; LIM domain; AP2; PBZB; zinc finger domain;	
KM	type 2 cytochrome; CCAAT box element; ATB.	
OS	Pinus radiata.	
PN	MO200053724-A2.	
XD	14-SEP-2000.	

XX 09-MAR-2000: 2000MO-US06112.
 PF 11-MAR-1999: 99US-0266513.
 PR 18-AUG-1999: 99US-0149485.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 PI Wood M, McGrath A, Shank M, Glenn M
 XI WPI: 2000-579369/54.
 DE New isolated polynucleotide encoding a plant transcription factor for
 PI producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 PT having modified gene expression or modified activity of a polypeptide
 PT
 XX
 PS Claim 8: Pages 430-431: 747pp: English.
 CC The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
 CC transcription factor. The transcription factor may be used to produce a
 CC plant having modified gene expression such as a woody plant e.g. a
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 CC to modify the activity of a polypeptide in a plant. The transcription
 CC factors of the present invention are members from the following families
 CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
 CC zipper, LIM domain, AP2 and ERBB, zinc finger domains of type 2
 CC CysH182, CCAT box elements and MYB.
 CC
 XI Sequence 119 AA:
 SO
 Query Match 84.98: Score 158: DB 21: Length 119:
 Best Local Similarity 86.18: Pred. No. 9.4e-17:
 Matches 31: Conservative 3: Mismatches 2: Indels 0: Gaps 0:
 07 1 KNIRRYDNLVLMNNISKEKIKWIGLPTNS 36
 DB 71 knirrydnlvlnmdllskkkelvgyipld 106
 RESULT 11
 AAB33007 standard; Protein: 120 AA.
 AC AAB33007:
 XI 25-JAN-2001 (first entry)
 DT
 DE Pinus radiata transcription factor protein sequence #134.
 XX
 XX Plant: transcription factor; gene expression; eucalyptus; pine; acacia;
 KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
 KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
 KW homeodomain zipper; LIM domain; AP2; ERBB; zinc finger domain;
 KW type 2 CysH182; CCAT box element; MYB.
 XX
 OS Pinus radiata.
 XX
 PN MO200053724-A2.
 PD 14-SEP-2000.
 XX 09-MAR-2000: 2000MO-US06112.
 PF 11-MAR-1999: 99US-0266513.
 PR 18-AUG-1999: 99US-0149485.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Wood M, McGrath A, Shank M, Glenn M;
 PI WPI: 2000-579369/54.
 DR
 XX
 PT New isolated polynucleotide encoding a plant transcription factor for
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 PT having modified gene expression or modified activity of a polypeptide
 PT
 XX
 PS Claim 8: Page 390: 747pp: English.
 CC The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
 CC transcription factor. The transcription factor may be used to produce a
 CC plant having modified gene expression such as a woody plant e.g. a
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 CC to modify the activity of a polypeptide in a plant. The transcription
 CC factors of the present invention are members from the following families
 CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
 CC zipper, LIM domain, AP2 and ERBB, zinc finger domains of type 2
 CC CysH182, CCAT box elements and MYB.
 CC
 XI Sequence 120 AA:
 SO
 Query Match 87.38: Score 153: DB 21: Length 120:
 Best Local Similarity 83.38: Pred. No. 5.7e-16:
 Matches 30: Conservative 4: Mismatches 2: Indels 0: Gaps 0:
 07 1 KNIRRYDNLVLMNNISKEKIKWIGLPTNS 36
 DB 70 knirrydnlvlnmdllskkkelvgyipld 105
 RESULT 12
 AAB33089 standard; Protein: 575 AA.
 ID AAB33089:
 AC AAB33089:
 XI 25-MAR-1999 (first entry)
 DT
 DE Caenorhabditis elegans synxv protein LIN-55.
 XX
 XX LIN-55: synthetic multivulva; Synxv; signal transduction;
 KW animal model; tumour suppressor; retinoblastoma; cancer; cancer;
 KW cell proliferation; gene therapy.
 XX
 OS Caenorhabditis elegans.
 XX
 PN MO9854299-A1.
 PD 03-DEC-1996.
 XX 26-MAY-1996: 98MO-US11043.
 PF 26-MAY-1997: 97US-0047996.
 PR
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY,
 PA
 PI Ceol C, Horvitz HR, Lu X;
 PI WPI: 1999-045362/04.
 DR N-PSDB: AAV72862.
 XX
 PT Novel LIN-37, -35, -55, -52, -53 and -54 gene from C. elegans -
 PT useful for treating diseases associated with altered levels of cell
 PT proliferation, e.g. carcinomas
 XX
 XX Claim 7: Fig 8: 70pp: English.

CC This is the amino acid sequence of Caenorhabditis elegans LIN-55, a
 CC novel homolog of the DP family of proteins that bind DNA at
 CC specific sites, thereby regulating the transcription of genes
 CC essential for cell cycle progression. The lin-55 gene (see
 CC AAV72862) is a novel synthetic multiviral (synhuv) gene involved in
 CC cell fate and proliferation, and is part of a pathway which may be
 CC used as a genetic and biochemical model system for tumour suppression
 CC and cancer in mammals. Synhuv pathway genes and proteins may be used
 CC to identify genes which are part of the mammalian pathway and to
 CC identify genes, proteins and therapeutic compounds which modulate
 CC this pathway. Pure nucleic acids (see AAV72839-65) encoding C.
 CC elegans Synhuv polypeptides selected from LIN-37, -35, -32, -31,
 CC -30, -29 and E2F-1 (see AAV72866-92), are new. Also claimed are:
 CC (1) nucleic acids (see AAV72866-67) encoding the mouse and human
 CC homologues of the C. elegans LIN-54; (2) vectors containing the
 CC nucleic acids; (3) transgenic cells; (4) a pure mammalian Synhuv
 CC polypeptide; and (5) an antibody which binds to a Synhuv family
 CC protein. The Synhuv nucleic acids and polypeptides can be used to
 CC diagnose and treat, especially by gene therapy, conditions
 CC involving altered levels of cell proliferation, e.g. Synhuv-
 CC associated carcinomas.

CC Sequence 573 AA:

Query Match 82.38; Score 153; DB 20; Length 573;
 Best Local Similarity 75.78; Pred. No. 3.8e-15;
 Matches 28; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 KNRIRRYDALNVLMAMNIRKREIKWIGLPTNSA 37
 DB 99 KNRIRRYDALNVLMAMNIRKREIKWIGLPTNSA 35

RESULT 13

ID AAV30507 standard; Peptide; 30 AA.

AC AAV30507;

DX 26-OCT-1998 (first entry)

DE DP-1 transcription factor antagonist peptide H7.

KX DP-1: transcription factor; antagonist; E2F protein; apoptosis;
 KW cell proliferation; cardiovascular cell; restenosis; tumour;
 XX surgical stent; therapy.

OS Synthetic.

OS Homo sapiens.

PH Key Location/Qualifiers

PT Peptide 3.9 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

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PT Peptide 5.15 /note- "Claim 3"

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PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT Peptide 5.15 /note- "Claim 3"

PT e.g. for preventing restenosis
 XX Claim 4; Page 44; 55pp; English.
 PS Peptide H7 comprises amino acid residues 170-199 in the DP box
 CC (1) (see AAV30501) of transcription factor DP1. Claimed peptides
 CC (1) (see AAV30501-07) containing one or both of 2 motifs (see
 CC AAV30502-03) of the DP box are capable of antagonizing the
 CC heterodimerization of a DP protein with an E2F protein. Also
 CC claimed are variants of these peptides, especially containing
 CC substitutions of residues corresponding to residues 167, 169, 171
 CC and 175 of DP-1, fusion proteins (11) comprising (1) or (11) and a
 CC membrane translocation sequence (see AAV30508), expression vectors
 CC encoding (1)-(11) and host cells. (1)-(11) are used
 CC therapeutically to induce apoptosis, specifically in tumour or
 CC cardiovascular cells, either in vivo or in vitro, e.g. for purging
 CC bone marrow. Surgical stents comprising (1)-(11) are used to
 CC treat or prevent restenosis in patients who have undergone
 CC angioplasty. (1)-(11) function by inactivating the DNA-binding
 CC activity of DP/E2F heterodimers. They are also used as research
 CC reagents, as positive controls in assays for identifying
 CC antagonists of DP-1/E2F dimerisation and as immunoscreening agents.
 CC Also described is the use of sequences antisense to nucleic acids
 CC encoding (1)-(11) to control DP levels in cells, particularly by
 CC gene therapy. When formulated with cytotoxic or cytostatic agents,
 CC (1)-(11) enhance cell killing.

CC Sequence 30 AA:

Query Match 81.74; Score 152; DB 19; Length 30;
 Best Local Similarity 100.00; Pred. No. 1.5e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 YDALNVLMAMNIRKREIKWIGLPTNSA 37

DB 1 ydalnvlmamnlrskelkhwlgptnsa 30

RESULT 14

ID AMG22852 standard; Protein; 277 AA.

AC AMG22852;

DX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 25937.

KX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridization assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

OS Arabidopsis thaliana.

OS Arabidopsis thaliana.

OS Arabidopsis thaliana.

OS Arabidopsis thaliana.

OS Arabidopsis thaliana.

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OS Arabidopsis thaliana.

Wed Aug 28 13:32:29 2002

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Query Match 81.2%; Score 151; DB 21; Length 277;
Best Local Similarity 83.3%; Pred. No. 3, 2e-15;
Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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OY 1 KNIRRYVDALNVLMANNISKEKEIRMGIPGTS 35
DB 44 KNIRRYVDALNVLMANNISKEKEIRMGIPGTS 79

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RESULT 15

AB07975 standard; Protein; 299 AA.

AB07975;

14-NOV-2000 (first entry)

A corn transcription factor designated DP.

DP polypeptide: transcription factor; gene transcription; cell cycle;

DNA replication; DRR; differentiation-regulated transcription factor 1;

transgenic plant; transformation efficiency.

See maye.

Key Location/Qualifiers

Misc-difference 1 /note="any amino acid encoded by NNN"

MO200047614-A1.

17-AUG-2000.

11-FEB-2000; 2000MO-US03651.

12-FEB-1999; 99US-0119857.

(PION-) PIONEER HI-BRED INT INC.

Lowe KS, Gordon-kamm NJ, Bailey MA, Gregory CA;

NPI: 2000-524530/47.

N-PSDB: AAA59702.

Transgenic plants comprising an expression cassette consisting of a DP

nucleic acid, when expressed, the nucleic acid increases the efficiency

of plant cell transformation by increasing the number of dividing cells

in the plant

Disclosure: Page 71-73; 76pp; English.

```

XX The present sequence represents a corn DP (not defined) polypeptide.
CC The polypeptide is a transcription factor that activates transcription
CC of numerous genes involved in DNA replication, thus playing a role in the
CC G1 to S transition in the cell cycle. Do, also called DRR
CC (differentiation-regulated transcription factor 1) has been shown to
CC form specific multiprotein complexes with the retinoblastoma
CC susceptibility protein, p107, cyclins and cdk2. The DP polynucleotide
CC was used to produce a transgenic plant. The DP nucleic acids and
CC proteins are useful for increasing transformation efficiency in plants
CC by increasing the number of dividing cells in the plant (dividing
CC cells may be more receptive to transformation).
XX
SQ Sequence 299 AA;

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Query Match 81.2%; Score 151; DB 21; Length 299;
Best Local Similarity 83.3%; Pred. No. 3, 5e-15;
Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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OY 1 KNIRRYVDALNVLMANNISKEKEIRMGIPGTS 36
DB 98 KNIRRYVDALNVLMANNISKEKEIRMGIPGTS 133

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Search completed: August 28, 2002, 12:59:14
Job time: 240 sec

Wed Aug 28 13:32:29 2002

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GenCore version 4.5
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On protein - protein search, using sw model

Run on: August 28, 2002, 12:59:34 ; Search time 10.33 Seconds

(without alignments)
138,686 Million cell updates/sec

Title: US-09-900-147-1

Perfect score: 186
Sequence: 1 RNRIRRYDALMTVMAMNITSKREKRIWGLPTNSA 37

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 3819550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	153	82.3	598	1	TPP1_MOUSE
6	98.5	53.0	446	1	TPP2_MOUSE
7	74.5	40.1	272	1	TPP1_MOUSE
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ALIGNMENTS

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45	47	25.3	356	1	CLPE_MOUSE

34	48	25.8	1928	1	MYSL_YEAST
35	47.5	25.5	594	1	PSA1_MOUSE
36	47.5	25.5	594	1	PSA1_MOUSE
37	47.5	25.5	615	1	SPPL_MOUSE
38	47.5	25.5	1335	1	SPPL_MOUSE
39	47.5	25.5	2032	1	CTOG_MOUSE
40	47.5	25.5	4568	1	CTOG_MOUSE
41	47	25.3	258	1	PAER_MOUSE
42	47	25.3	263	1	CLPE_MOUSE
43	47	25.3	356	1	CLPE_MOUSE
44	47	25.3	356	1	CLPE_MOUSE
45	47	25.3	356	1	CLPE_MOUSE

34	48	25.8	1928	1	MYSL_YEAST
35	47.5	25.5	594	1	PSA1_MOUSE
36	47.5	25.5	594	1	PSA1_MOUSE
37	47.5	25.5	615	1	SPPL_MOUSE
38	47.5	25.5	1335	1	SPPL_MOUSE
39	47.5	25.5	2032	1	CTOG_MOUSE
40	47.5	25.5	4568	1	CTOG_MOUSE
41	47	25.3	258	1	PAER_MOUSE
42	47	25.3	263	1	CLPE_MOUSE
43	47	25.3	356	1	CLPE_MOUSE
44	47	25.3	356	1	CLPE_MOUSE
45	47	25.3	356	1	CLPE_MOUSE

34	48	25.8	1928	1	MYSL_YEAST
35	47.5	25.5	594	1	PSA1_MOUSE
36	47.5	25.5	594	1	PSA1_MOUSE
37	47.5	25.5	615	1	SPPL_MOUSE
38	47.5	25.5	1335	1	SPPL_MOUSE
39	47.5	25.5	2032	1	CTOG_MOUSE
40	47.5	25.5	4568	1	CTOG_MOUSE
41	47	25.3	258	1	PAER_MOUSE
42	47	25.3	263	1	CLPE_MOUSE
43	47	25.3	356	1	CLPE_MOUSE
44	47	25.3	356	1	CLPE_MOUSE
45	47	25.3	356	1	CLPE_MOUSE

34	48	25.8	1928	1	MYSL_YEAST
35	47.5	25.5	594	1	PSA1_MOUSE
36	47.5	25.5	594	1	PSA1_MOUSE
37	47.5	25.5	615	1	SPPL_MOUSE
38	47.5	25.5	1335	1	SPPL_MOUSE
39	47.5	25.5	2032	1	CTOG_MOUSE
40	47.5	25.5	4568	1	CTOG_MOUSE
41	47	25.3	258	1	PAER_MOUSE</

CC BRAIN, PLACENTA, LIVER AND KIDNEY. LOWER LEVELS IN LUNG AND
 CC PANCREAS. NOT DETECTED IN HEART.
 CC -1- INDUCTION: DOWN-REGULATED DURING DIFFERENTIATION.
 CC -1- PFM: PHOSPHORYLATION BY E2F-1-BOUND CYCLIN A-CDK2, IN THE S PHASE,
 CC INHIBITS E2F-MEDIATED DNA BINDING AND TRANSCRIPTION.
 CC -1- MISCELLANEOUS: E2F/DP TRANSCRIPTION CAN BE MEDIATED BY SEVERAL
 CC COFACTORS INCLUDING TBP, TFIIF, MDM2 AND CBP.
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: L33959; AA58440.1; .
 CC HSP: Q14188; ICF7.
 CC DR HSP: 189902; .
 CC DR InterPro: IPR003316; E2F_TDP.
 CC DR Pfam: PF02319; E2F_TDP; 1.
 CC KN Transcription regulation; DNA-binding; Activator; Nuclear protein;
 CC Phosphorylation; Cell cycle.
 CC PT DNA_BIND 113 195 POTENTIAL.
 CC PT DOMAIN 161 195 DEF BOX.
 CC PT DOMAIN 204 277 DIMERIZATION (POTENTIAL).
 CC PT DOMAIN 214 246 DCB1.
 CC PT DOMAIN 239 315 DCB2.
 CC PT DOMAIN 211 327 ENHANCER BINDING OF RB PROTEIN TO E2F.
 CC PT DOMAIN 250 253 POLY-PRO.
 CC PT DOMAIN 394 410 ASP/GLU-RICH (ACIDIC) (NCB DOMAIN).
 CC PT MOO_RES 23 23 PHOSPHORYLATION (BY CDK2) (POTENTIAL).
 CC SEQUENCE 410 AA; 45070 MW; 3FEEF1B89D9D0 CRC64;

Query Match 100.00; Score 186; DB 1; Length 410;
 Best Local Similarity 100.00; Pred. No. 9.2e-19;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRYDALNVLANMNIKKREKINIGLPTNSA 37
 DB 163 KNIRRYDALNVLANMNIKKREKINIGLPTNSA 199

RESULT 2
 TDP1_MOUSE STANDARD; PRT: 410 AA.
 AC 008619;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE Transcription factor DP-1 (E2F dimerization partner 1) (DRTF1-
 DE polypeptide-1).
 GN TDP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID:10090;
 RN (1)
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE-9318867; PubMed-446173;
 RA Gilling R., Partridge J.F., Bandaru L.R., Totty N.F.,
 RA Haux J., La Thangue N.B.,
 RT "A new component of the transcription factor DRTF1/E2F."
 RT Nature 362:83-87(1993).
 RL (2)
 RP REVISIONS TO C-TERMINAL.
 RA Gilling R.,
 RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE-98025478; PubMed-9376316;

RA Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L.,
 RA Philippe R.A.;
 RA "Expression patterns of the E2F family of transcription factors during
 RA mouse nervous system development."
 RA Mech. Dev. 66:13-25(1997).
 RP (4)
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE-97294022; PubMed-9149906;
 RA Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L.,
 RA Philippe R.A.;
 RA "Expression patterns of the E2F family of transcription factors
 RA during murine epithelial development."
 RA Cell Growth Differ. 8:553-561(1997).
 RL Cell Growth Differ. 8:553-561(1997).
 CC -1- FUNCTION: CAN STIMULATE E2F-DEPENDENT TRANSCRIPTION. BINDS DNA
 CC COOPERATIVELY WITH E2F FAMILY MEMBERS THROUGH THE E2 RECOGNITION
 CC SITE. TTCC/CCGC, FOUND IN THE PROMOTER REGION OF A NUMBER OF
 CC GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OR IN
 CC DNA REPLICATION. THE DP2/E2F COMPLEX FUNCTIONS IN THE CONTROL OF
 CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E2F-1/DP COMPLEX
 CC APPEARS TO MEDiate BOTH CELL PROLIFERATION AND APOPTOSIS.
 CC -1- SUBUNIT: COMPONENT OF THE DRTF1/E2F TRANSCRIPTION FACTOR COMPLEX.
 CC FORMS HETERODIMERS WITH E2F FAMILY MEMBERS. THE COMPLEX CAN
 CC INTERACT WITH HYPOPHOSPHORYLATED RETINOBLASTOMA PROTEIN RB1 AND
 CC RELATED PROTEINS (P107 AND P130) THAT INHIBIT THE E2F
 CC TRANSCRIPTIONAL DOMAIN. DURING THE CELL CYCLE, RB BECOMES
 CC PHOSPHORYLATED IN MID-TO-LATE G1 PHASE, DETACHES FROM THE
 CC DRTF1/E2F COMPLEX RENDERING E2F TRANSCRIPTIONALLY ACTIVE. VIRAL
 CC ONCOPROTEINS, NOTABLY E1A, T-ANTIGEN AND HPV E7, ARE CAPABLE OF
 CC SEQUESTERING RB PROTEIN, THUS RELEASING THE ACTIVE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: IN THE INTESTINAL EPITHELIUM, FIRST EXPRESSED
 CC IN UNDIFFERENTIATED AND MESODERMAL TISSUES, LEVELS INCREASING BY
 CC 12.5 DPC IN THE EPITHELIAL COMPARTMENT, WITH EPITHELIAL
 CC DIFFERENTIATION AT 15.5 DPC. DP-1 EXPRESSION INCREASES
 CC SUBSTANTIAL IN THE INTERVILLUS EPITHELIUM WITH LOWER LEVELS IN
 CC THE MESENTERIC. AT LATER STAGES, EXPRESSION CONTINUES IN THE
 CC INTERVILLUS EPITHELIUM. ALSO FOUND AT LOWER LEVELS IN THE
 CC DEVELOPING VILLI. IN THE DEVELOPING BRAIN, HIGHEST LEVELS FOUND
 CC BETWEEN 11.5 AND 13.5 DPC IN THE VENTRICULAR REGION. IN THE
 CC DEVELOPING RETINA, DP-1 IS EXPRESSED BOTH IN RETINOBLAST AND
 CC GAMGANGION CELL LAYERS FROM 14.5 DPC TO 6 DAYS AFTER BIRTH. IN OTHER
 CC DEVELOPING TISSUES, DP-1 EXPRESSION IS HIGHEST IN THE THYMUS. ALSO
 CC PRESENT IN KIDNEY, LUNG, LIVER, HEART AND CHONDROCYTES. WEAKLY
 CC EXPRESSED IN SKELETAL MUSCLE AND ABSENT FROM CHONDROID FLEXUS.
 CC -1- PHOSPHORYLATION BY E2F-1-BOUND CYCLIN A-CDK2, IN THE S PHASE,
 CC INHIBITS E2F-MEDIATED DNA BINDING AND TRANSCRIPTION.
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
 CC -----
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 CC -----
 CC EMBL: X72310; CA51056.1; .
 CC HSP: Q14188; ICF7.
 CC DR HSP: 189902; .
 CC DR InterPro: IPR003316; E2F_TDP.
 CC DR Pfam: PF02319; E2F_TDP; 1.
 CC KN Transcription regulation; DNA-binding; Activator; Nuclear protein;
 CC Phosphorylation; Cell cycle.
 CC PT DNA_BIND 113 195 POTENTIAL.
 CC PT DOMAIN 161 195 DEF BOX.
 CC PT DOMAIN 204 277 DIMERIZATION (POTENTIAL).
 CC PT DOMAIN 214 246 DCB1.
 CC PT DOMAIN 239 315 DCB2.
 CC PT DOMAIN 211 327 POLY-PRO.
 CC PT DOMAIN 394 410 ASP/GLU-RICH (ACIDIC) (NCB DOMAIN).
 CC PT MOO_RES 23 23 PHOSPHORYLATION (BY CDK2) (POTENTIAL).
 CC SEQUENCE 410 AA; 45230 MW; FEEA90C78107189 CRC64;

Query Match 100.0%; Score 186; DB 1; Length 410;
 Best Local Similarity 100.0%; Pred. No. 9, 2e-15;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KNIRRYVDALVLMANNISKEKKEIKWGLPTNSA 37
 ||||||||||||||||||||||||||||||||||||
 DB 163 KNIRRYVDALVLMANNISKEKKEIKWGLPTNSA 169

RESULT 3
 TDP2_HUMAN STANDARD; PRT; 446 AA.
 AC Q14188; Q14187; Q13331;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transcription factor DP-2 (E2F dimerization partner 2).
 GN TDP2 OR DP2
 OS Homo sapiens (human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NB1_TaxID=9606;
 (1)
 NP SEQUENCE FROM N.A. (DELTA ISOFORM), AND CHARACTERIZATION.
 RA MEDLINE-95357935; PubMed-779537;
 RA Hu C.L., Sukerberg L.R., Ngwu C., Harlow E., Lees J.A.;
 RT "In vivo association of E2F and DP family proteins.";
 RL Mol. Cell. Biol. 15:2536-2546(1995).
 (2)
 NP SEQUENCE FROM N.A. (DELTA ISOFORM).
 RA Zhang Y., Chellappan S.P.;
 RT "Transcriptional activation and expression of DP transcription
 factor during cell cycle and TPA-induced U937 differentiation.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBS databases.
 (3)
 NP SEQUENCE OF 63-79 FROM N.A. (DELTA ISOFORM), AND ALTERNATIVE SPLICING.
 RA TISSUE-NerveTissue;
 RA MEDLINE-96353862; PubMed-8755520;
 RA Rogers K.T., Higgins P.D.R., Milla M.M., Phillips R.S., Horowitz J.M.;
 RT "DP-2, a heterodimeric partner of E2F: identification and
 characterization of DP-2 proteins expressed in vivo.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7594-7599(1996).
 (4)
 NP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 121-215.
 RA MEDLINE-99190701; PubMed-10090723;
 RA Zheng M., Freeman E., Pabo C.O., Pavletich N.P.;
 RT "Structural basis of DNA recognition by the heterodimeric cell cycle
 transcription factor E2F-DP.";
 RL Genes Dev. 13:666-674(1999).
 (5)
 NP FUNCTION: CAN STIMULATE E2F-DEPENDENT TRANSCRIPTION. BINDS DNA
 COOPERATIVELY WITH E2F FAMILY MEMBERS THROUGH THE E2 RECOGNITION
 SITE. TTTC/GCC, FOUND IN THE PROMOTER REGION OF A NUMBER OF
 GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OR IN
 DNA REPLICATION. THE DP2/E2F COMPLEX FUNCTIONS IN THE CONTROL OF
 CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E2F-1/DP COMPLEX
 APPEARS TO REGULATE BOTH CELL PROLIFERATION AND APOPTOSIS.
 (6)
 NP SUBUNIT: COMPONENT OF THE DP2/22P TRANSCRIPTION FACTOR COMPLEX.
 (7)
 NP FORMS HETERODIMERS WITH E2F FAMILY MEMBERS. THE COMPLEX CAN
 INTERACT WITH HYPHOSPHORYLATED RETINOBLASTOMA PROTEIN RB1 AND
 RELATED PROTEINS (P107 AND P130) THAT INHIBIT THE E2F
 TRANSACTIVATION DOMAIN. DURING THE CELL CYCLE, RB BECOMES
 PHOSPHORYLATED IN MID-TO-LATE G1 PHASE, DETACHES FROM THE
 DP2/22P COMPLEX RENDERING E2F TRANSCRIPTIONALLY ACTIVE. VIRAL
 ONCOPROTEINS, NOTABLY E1A, T-ANTIGEN AND SV40 E7, ARE CAPABLE OF

SEQUENCING RB PROTEIN, THUS RELEASING THE ACTIVE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: At least 4 ISOFORMS: ALPHA/49 KDA (SHOWN
 HERE), BETA/43 KDA, GAMMA AND DELTA/48 KDA. MAY BE PRODUCED BY
 ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGH LEVELS IN HEART AND SKELETAL MUSCLE. ALSO
 FOUND IN PLACENTA, KIDNEY, BRAIN, LUNG AND LIVER. THE PRESENCE AS
 WELL AS THE ABUNDANCE OF THE DIFFERENT TRANSCRIPTS APPEAR TO
 VARY SIGNIFICANTLY IN DIFFERENT TISSUES AND CELL LINES.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
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 or send an email to license@1sb-rib.ch).
 CC EMBL; L40386; AA65016.1;
 CC EMBL; U18422; AB60378.1;
 CC EMBL; U75488; AB37321.1;
 CC EMBL; U75117; AAC50642.1;
 CC PDB; 1CP7; 02-APR-99.
 CC TRANSFAC; T03000;
 CC MIM; 602160;
 CC InterPro; IPR003316; E2F_TDP.
 CC Pfam; PF02320; E2F_TDP; 1.
 CC Transcription regulation; DNA-binding; Activator; Nuclear protein;
 CC Phosphorylation; Cell cycle; Alternative splicing; 3D-structure.
 CC DNA_BIND 129 210 DEF BOX
 FT DOMAIN 219 292
 FT DOMAIN 229 261 DCB1
 FT DOMAIN 274 330
 FT DOMAIN 432 446 ASP/GLU-RICH (ACIDIC) (NCB DOMAIN).
 FT MOD_RES 24 24 PHOSPHORYLATION (BY CDK2) (POTENTIAL).
 FT MOD_RES 42 42 PHOSPHORYLATION (BY CDK2) (POTENTIAL).
 FT VARSPIC 1 61 MISSING (IN ISOFORM BETA, ISOFORM GAMMA
 AND ISOFORM DELTA).
 FT VARSPIC 103 118 MISSING (IN ISOFORM BETA AND ISOFORM
 GAMMA).
 FT VARSPIC 173 173 S -> SQ (IN ISOFORM GAMMA).
 FT VARIANT 64 64 I -> T.
 FT VARSPIC 173 173 /FTID=VAR_002272.
 FT SEQUENCE 446 AA; 49236 MW; 19AC685BADA61DFE1 CRC64;

Query Match 100.0%; Score 186; DB 1; Length 446;
 Best Local Similarity 100.0%; Pred. No. 1e-18;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KNIRRYVDALVLMANNISKEKKEIKWGLPTNSA 37
 ||||||||||||||||||||||||||||||||||||
 DB 178 KNIRRYVDALVLMANNISKEKKEIKWGLPTNSA 214

RESULT 4
 TDP2_HUMAN STANDARD; PRT; 377 AA.
 AC Q24318;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Transcription factor DP.
 GN DP.
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NC NB1_TaxID=7227;
 (1)

SEQUENCE FROM N.A.
 TISSUE-Dye Imaginal disk;
 MEDLINE-94294381; PubMed-8022787;
 RA Dylachet B., Brook A., Dembakl M., Yenush L., Dyson N.;
 "DNA-binding and trans-activation properties of Drosophila E2F and DP
 proteins";
 Proc. Natl. Acad. Sci. U.S.A. 91:6359-6363(1994).
 CC -1- FUNCTION: CAN STIMULATE E2F-DEPENDENT TRANSCRIPTION.
 CC -1- SUBUNIT: HETEROOLIGOMER OF E2F AND DP COOPERATE TO GIVE SEQUENCE-
 CC SPECIFIC DNA BINDING AND OPTIMAL TRANS-ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potentially).
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
 CC
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DR EMBL: X79708; CA55147.2; ALT_INT.
 DR HSP: Q1188; ICF7.
 DR Flybase: FBgn0011763; DP.
 DR InterPro: IPR003116; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 81 88 POLY-SER.
 SO SEQUENCE 377 AA; 42663 MW; 868F180243C3DC CRC64.

Query Match 82.38; Score 166; DB 1; Length 377;
 Best Local Similarity 86.11; Pred. No. 5,6e-16;
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KNIRRVYDALVLMANNISKEKIKNGLP7NS 36
 DB 145 KNIRRVYDALVLMANNISKEKIKNGLP7NS 180

RESULT 5
 TOPH_CAREL STANDARD; PRT; 598 AA.
 AC 023703;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Transcription factor DP homolog.
 GN T2367.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditidae; Rhabditoidae;
 OC Rhabditidae; Peldoderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Bellore K.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ database.
 RM (2)
 REVISIONS.
 RC STRAIN-BRISTOL N2;
 RA Dublin R.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ database.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potentially).
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
 CC
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CC EMBL: I68319; CA93699.1;
 DR HSP: Q14188; ICF7.
 DR Wormpep: T2367.1; CE03702.
 DR InterPro: IPR003116; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 DR Hypothetical protein: Transcription regulation; DNA-binding;
 DR Nuclear protein.
 SO SEQUENCE 598 AA; 67930 MW; A79692087F3D3DAS CRC64;

Query Match 82.38; Score 153; DB 1; Length 598;
 Best Local Similarity 75.75; Pred. No. 6,3e-14;
 Matches 28; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 KNIRRVYDALVLMANNISKEKIKNGLP7NS 37
 DB 122 KNIRRVYDALVLMANNISKEKIKNGLP7NS 158

RESULT 6
 TOP2_MOUSE STANDARD; PRT; 446 AA.
 AC 06163;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transcription factor DP-2 (E2F dimerization partner 2) (DP-3).
 GN TPDP2 OR DP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC Tissue-brain, and kidney;
 RX MEDLINE-96038871; PubMed-7478568;
 RA Oromondroyd E., De La Lanza S., La Thangue N.B.;
 "A new member of the DP family, DP-3, with distinct protein products
 RT suggests a regulatory role for alternative splicing in the cell cycle
 RT transcription factor DP2/2P2";
 Oncogene 11:1437-1446(1995).
 RL
 CC -1- FUNCTION: CAN STIMULATE E2F-DEPENDENT TRANSCRIPTION. BINDS DNA
 CC COOPERATIVELY WITH E2F FAMILY MEMBERS THROUGH THE E2 RECOGNITION
 CC SITE. TTCC/GCCC, FOUND IN THE PROMOTER REGION OF A NUMBER OF
 CC GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OR IN
 CC DNA REPLICATION. THE DP2/E2F COMPLEX FUNCTIONS IN THE CONTROL OF
 CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E2F-1/DP COMPLEX
 CC APPEARS TO MEDiate BOTH CELL PROLIFERATION AND APOPTOSIS.
 CC -1- SUBUNIT: COMPONENT OF THE DP2/E2F TRANSCRIPTION FACTOR COMPLEX.
 CC FORMS HETEROOLIGOMERS WITH E2F FAMILY MEMBERS. THE COMPLEX CAN
 CC INTERACT WITH HYPOHOSPHORYLATED RETINOBLASTOMA PROTEIN RB1 AND
 CC RELATED PROTEINS (P107 AND P130) THAT INHIBIT THE E2F
 CC TRANSCRIPTIONAL DOMAIN. DURING THE CELL CYCLE, RB BECOMES
 CC PHOSPHORYLATED IN MULTIPLE SITES, RELEASING E2F TRANSCRIPTIONALLY ACTIVE. VITAL
 CC DP2/E2F COMPLEX, RELEASING E2F TRANSCRIPTIONALLY ACTIVE. VITAL
 CC ONCOPROTEINS, NOTABLY E1A, T-ANTIGEN AND HPV E7, ARE CAPABLE OF
 CC SEQUESTERING RB PROTEIN, THUS RELASING THE ACTIVE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS, ALPHA (SHOWN HERE),
 CC BETA, GAMMA AND DELTA, ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED. HIGHEST
 CC LEVELS IN SPLEEN AND HEART.
 CC -1- PTM: PHOSPHORYLATION BY E2F-1-BOUND CYCLIN A-COR2, IN THE S PHASE,
 CC INHIBITS E2F-MEDIATED DNA BINDING AND TRANS-ACTIVATION.
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
 CC
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CC EMBL: S79780; MB35506.2;

DR HSSP: Q14188; ICF7.

DR MGD: MG1:107167; TdP2.

DR InterPro: IPR00316; E2F.TDP.

DR Pfam: PF02319; E2F.TDP. 1.

DR Transcription regulation; DNA-binding; Activator; Nuclear protein;

DR Phosphorylation; Cell cycle; Alternative splicing.

RT DNA_BIND 129 210 POTENTIAL.

RT DOMAIN 118 210 DEF BOX.

RT DOMAIN 219 292 DIMERIZATION (POTENTIAL).

RT DOMAIN 229 261 DCB1.

RT DOMAIN 274 330 DCB2.

RT DOMAIN 432 446 ASP/GLU-RICH (ACIDIC) (NCB DOMAIN).

RT MOD_RES 24 24 PHOSPHORYLATION (BY CDK2) (POTENTIAL).

RT MOD_RES 42 42 PHOSPHORYLATION (BY CDK2) (POTENTIAL).

RT VARSPIC 1 61 MISSING (IN ISOFORM BETA, ISOFORM GAMMA AND ISOFORM DELTA).

RT VARSPIC 103 118 MISSING (IN ISOFORM BETA AND ISOFORM GAMMA).

RT VARSPIC 173 173 S -> SQ (IN ISOFORM GAMMA).

RT SEQUENCE 466 AA; 49098 MW; 05687AC88B2FE8A CRC64;

Query Match 53.0%; Score 98.5; DB 1; Length 446;
Best Local Similarity 67.6%; Pred. No. 2.3e-06;
Matches 23; Conservative 1; Mismatches 1; Indels 9; Gaps 1;

1 KNIRRYDALNVLMVLMNITSKKKEIKWIGLPT 34
DB 178 ENIRRYDALNVLMVLMNITSKKKEIKWIGLPT 34

RESULT 7
E2F6_MOUSE STANDARD; PRT: 272 AA.
AC 034917;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription factor E2F6 (E2F-6) (E2F-binding site modulating activity protein) (BMA).
GN E2F6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
DX NCBI_TaxID=10090;
NM (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98065940; Pubmed=9403682;
RA Moriel M., Venzel J., Bannister A.J., Kouzarides T., Hagerglaser C.;
RT "An E2F-1-like repressor of transcription."
RL Nature 390:567-586(1997).
CC -1- FUNCTION: INHIBITOR OF E2F-DEPENDENT TRANSCRIPTION. BINDS DNA COOPERATIVELY WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE, TTTC/CCGC. HAS A PREFERENCE FOR THE TTTC/CCGC E2F RECOGNITION SITE (BY SIMILARITY). EXHIBITS NO TRANSCRIPTIONAL ACTIVITY. APPEARS TO REGULATE A SUBSET OF E2F-DEPENDENT GENES WHOSE PRODUCTS ARE REQUIRED FOR ENTRY INTO THE CELL CYCLE BUT NOT FOR NORMAL CELL CYCLE PROGRESSION. OVEREXPRESSION DELAYS THE EXIT OF CELLS FROM THE S-PHASE (BY SIMILARITY).
CC -1- SUBUNIT: COMPONENT OF THE DRP1/E2F TRANSCRIPTION FACTOR COMPLEX.
CC -1- FORMS HETERODIMERS WITH DP FAMILY MEMBERS.
CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
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entities requires a license agreement (See <http://www.lab-sib.ch/announce/> or send an email to license@lab-sib.ch).

CC EMBL: AF032131; AAC53521.1;

DR HSSP: O16254; ICF7.

DR TRANSFAC: T03250;

DR MGD: MG1:1354159; E2F6.

DR InterPro: IPR00316; E2F.TDP.

DR Pfam: PF02319; E2F.TDP. 1.

DR Transcription regulation; DNA-binding; Repressor; Nuclear protein;

RT Cell cycle.

RT DOMAIN 1 62 BINDING TO CO-REPRESSORS (PROBABLE).

RT DNA_BIND 50 129 POTENTIAL.

RT DOMAIN 95 129 DEF BOX.

RT DOMAIN 130 222 DIMERIZATION (POTENTIAL).

RT DOMAIN 143 164 LECTINE-ZIPPER.

RT DOMAIN 173 272 TRANSCRIPTION REPRESSION DOMAIN (BY SIMILARITY).

RT SEQUENCE 272 AA; 30882 MW; CF42553DBADB8D CRC64;

Query Match 40.1%; Score 74.5; DB 1; Length 272;
Best Local Similarity 44.1%; Pred. No. 0.0031;
Matches 15; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

4 RRRRYDALNVLMVLMNITSKKKEIKWIGLPTNS 36
DB 100 KRRYDYNVGLGIELVEKSKMHRNIGSDLNW 133

RESULT 8
E2F6_HUMAN STANDARD; PRT: 281 AA.
AC 073461; 060544;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription factor E2F6 (E2F-6).
GN E2F6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
DX NCBI_TaxID=9606;
NM (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98356133; Pubmed=9689056;
RA Gaubatz S., Wood J.D., Livingston D.M.;
RT "Unusual proliferation arrest and transcriptional control properties of a newly discovered E2F family member, E2F-6."
RL Proc. Natl. Acad. Sci. U.S.A. 95:9190-9195(1998).
NM (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=98368635; Pubmed=9704927;
RA Cartright P., Mueller M., Hagerglaser C., Holm K., Helin K.;
RT "E2F-6: a novel member of the E2F family is an inhibitor of E2F-dependent transcription."
RL Oncogene 17:611-623(1998).
NM (3)
RP SEQUENCE OF 7-281 FROM N.A.
RX TISSUE=retal brain;
RX MEDLINE=98169460; Pubmed=9501179;
RA Tlraorch J.M., Fairchild B., Verona R., Moberg K., Andon N., Lees J.A.;
RT "E2F-6, a member of the E2F family that can behave as a transcriptional repressor."
RL Proc. Natl. Acad. Sci. U.S.A. 95:2850-2855(1998).
CC -1- FUNCTION: INHIBITOR OF E2F-DEPENDENT TRANSCRIPTION. BINDS DNA COOPERATIVELY WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE, TTTC/CCGC. HAS A PREFERENCE FOR THE TTTC/CCGC E2F RECOGNITION SITE. E2F-6 LACKS THE TRANSCRIPTIONAL ACTIVATION AND POCKET PROTEIN BINDING DOMAINS. APPEARS TO REGULATE A SUBSET OF E2F-DEPENDENT GENES WHOSE PRODUCTS ARE REQUIRED FOR ENTRY INTO THE CELL CYCLE BUT NOT FOR NORMAL CELL CYCLE PROGRESSION.

Best local similarity 43.8%; Pred. No. 0.014;
 Matches 14; Conservative 8; Mismatches 9; Indels 1; Gaps 1;
 4 BRAYDALYANIANINISKE-KREKICIGTPT 34
 111 111 111 111 111 111 111 111 111 111
 DB 159 KRRIIDIRNYEGLOIAKSKMNIOWIASRT 190

RESULT 10
 E2F1_HUMAN STANDARD; PRT; 437 AA.
 AC 001034; 032768; 013143;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Transcription factor E2F1 (E2F-1) (Retinoblastoma binding protein 3)
 DE (RbBP-3) (Pre-binding protein E2F-1) (PBB3) (Retinoblastoma-associated
 protein 3) (RbBP-1).
 CH E2F1 OR RbBP3.
 CS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 NM (1)
 NP SEQUENCE FROM M.A.
 RX MEDLINE-92346720; PubMed-1638634;
 RT Helin K., Lees J.A., Vidal M., Dyson M.J., Harlow E., Pattney A.;
 RT "A cDNA encoding a pre-binding protein with properties of the
 RT cell 70:331-350(1992).
 RL Cell 70:331-350(1992).
 NM (2)
 NP SEQUENCE FROM M.A.
 RX MEDLINE-92346721; PubMed-1638635;
 RT Keelin M.G., Jr., Krez M., Sellers W.R., Decaprio J.A., Achenbaum P.,
 RT Puche C.S., Chittenden T., Li Y., Farnham P.J., Blaser M.A.,
 RT Livingston D.M., Livingston E.K.;
 RT "Expression cloning of a cDNA encoding a retinoblastoma-binding
 RT protein with E2F-like properties.";
 RT Cell 70:351-364(1992).
 RL Cell 70:351-364(1992).
 NM (3)
 NP SEQUENCE FROM M.A.
 RX MEDLINE-91078763; PubMed-1448092;
 RT Shan B., Zhu X., Chen P., Dutta T., Yang Y., Sharp D., Lee W.H.;
 RT "Molecular cloning of cellular genes encoding
 RT retinoblastoma-associated proteins: identification of a gene with
 RT properties of the transcription factor E2F.";
 RT Mol. Cell. Biol. 12:5620-5631(1992).
 RL Mol. Cell. Biol. 12:5620-5631(1992).
 NM (4)
 NP SEQUENCE FROM M.A.
 RX MEDLINE-97082961; PubMed-8964493;
 RT Neuman E., Sellers W.R.S., McNeil J.A., Lawrence J.B.,
 RT Keelin M.G., Jr.;
 RT "Structure and partial genomic sequence of the human E2F1 gene.";
 RT Gene 173:153-169(1996).
 RL Gene 173:153-169(1996).
 NM SEQUENCE FROM M.A.
 RX Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RX Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RX Bailey J., Barlow K.F., Bates K.N., Beard L.N., Beare D.M.,
 RX Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RX Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
 RX Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RX Clegg S., Cobley V.E., Collier R.E., Connor F., Corby M.R.,
 RX Coulson A., Coville G.J., Dendean R., Dhami F., Dunn M.R.,
 RX Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RX Grafton D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RX Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RX Huckle E., Hunt A.R., Hunt S.E., Jerchow K., Johnson K., Johnson D.,
 RX Kay M.P., Kimberley A.M., King A., Knight K., Laird G.R., Lavelle S.,
 RX Lehar V.L., Martin I., Leverhew M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RX Marsh V.L., Martin S.L., McManus L.J., McMay K., McWhirry A.A.,
 RX Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RX Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

Phillimore B.J.C.T., Prichard J., Prichard S.R., Plumb R.W., Ramsay M.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Shue C.D., Smith M.T., Soderlund C., Steward C.A., Sultana J.B.,
 RA Swan M., Symons M., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Troiano A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitehead P., Willey D.E., Williams L., Williams S.A.,
 RA Wiltshire L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RA "The DNA sequence and comparative analysis of human chromosome 20.";
 RA Nature 416:865-871(2001).
 RL Nature 416:865-871(2001).
 NM (5)
 NP SEQUENCE OF 1-111 FROM M.A.
 RX MEDLINE-95047311; PubMed-7958836;
 RT Johnson D.G., Ohtani K., Nevins J.R.;
 RT "Autoregulatory control of E2F1 expression in response to positive
 RT and negative regulators of cell cycle progression.";
 RT Genes Dev. 8:1514-1525(1994).
 RL Genes Dev. 8:1514-1525(1994).
 NM (6)
 NP PHOSPHORYLATION.
 RX MEDLINE-95140412; PubMed-7838323;
 RA Kitagawa M., Higashi H., Suzuki-Takahashi I., Segawa K., Hanke S.R.,
 RA Taya Y., Nishimura S., Okuyama A.;
 RA "Phosphorylation of E2F-1 by cyclin A-cdk2.";
 RA Oncogene 10:229-236(1995).
 RL Oncogene 10:229-236(1995).
 NM (7)
 NP CYCLIN A/CDK2 BINDING DOMAIN.
 RX MEDLINE-94306513; PubMed-8033308;
 RA Krez M., Swan M.E., Shirokber S., Arany Z., Keelin M.G., Jr.,
 RA Livingston D.M.;
 RA "Negative regulation of the growth-promoting transcription factor
 RA E2F-1 by a stably bound cyclin A-dependent protein kinase.";
 RA Cell 78:161-172(1994).
 RL Cell 78:161-172(1994).
 NM (8)
 NP DIFFERENTIAL REGULATION BY CYCLIN/CDK2 KINASES.
 RX MEDLINE-95047332; PubMed-7958856;
 RA Dynlacht B.D., Flores O., Lees J.A., Harlow E.;
 RA "Differential regulation of E2F transcription by cyclin/cdk2
 RA complexes.";
 RA Genes Dev. 8:1772-1786(1994).
 RL Genes Dev. 8:1772-1786(1994).
 NM (9)
 NP REGULATION BY CYCLIN-DEPENDENT KINASES.
 RX MEDLINE-97343624; PubMed-9199321;
 RA Dynlacht B.D., Morberg K., Lees J.A., Harlow E., Zhu L.;
 RA "Specific regulation of E2F family members by cyclin-dependent
 RA kinases.";
 RA Mol. Cell. Biol. 17:3867-3875(1997).
 RL Mol. Cell. Biol. 17:3867-3875(1997).
 NM (10)
 NP INHIBITION OF DNA-BINDING.
 RX MEDLINE-95059071; PubMed-7969176;
 RA Xu M., Sheppard K.A., Peng C.-Y., Yee A.S., Plautz-Worms M.;
 RA "Cyclin A/CDK2 binds directly to E2F-1 and inhibits the DNA-binding
 RA activity of E2F-1/DP-1 by phosphorylation.";
 RA Mol. Cell. Biol. 14:8420-8431(1994).
 RL Mol. Cell. Biol. 14:8420-8431(1994).
 NM (11)
 NP FUNCTION IN APOPTOSIS.
 RX MEDLINE-94224788; PubMed-8170934;
 RA Wu X., Levine A.J.;
 RA "p53 and E2F-1 cooperate to mediate apoptosis.";
 RA Proc. Natl. Acad. Sci. U.S.A. 91:3602-3606(1994).
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3602-3606(1994).
 NM (12)
 NP TRANSCRIPTION INHIBITION.
 RX MEDLINE-94019124; PubMed-8413249;
 RA Helin K., Harlow E., Pattney A.;
 RA "Inhibition of E2F-1 transcription by direct binding of the
 RA retinoblastoma protein.";
 RA Mol. Cell. Biol. 13:6501-6508(1993).
 RL Mol. Cell. Biol. 13:6501-6508(1993).
 NM (13)
 NP FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY
 WITH DP PROTEIN THROUGH THE E2 RECOGNITION SITE. PPVCC/CCG;
 FOUND IN THE PROMOTER REGION OF A NUMBER OF GENES WHOSE PRODUCTS
 ARE INVOLVED IN CELL CYCLE REGULATION OR IN DNA REPLICATION. THE
 DRE1/E2F COMPLEX FUNCTIONS IN THE CONTROL OF CELL-CYCLE
 PROGRESSION FROM G1 TO S PHASE. E2F-1 BINDS PREFERENTIALLY R81
 PROTEIN, IN A CELL-CYCLE DEPENDENT MANNER. IT CAN MEDIATE BOTH

DE Transcription factor E2F2 (E2F-2).
 CC E2F2.
 CC Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID=9606;
 CC (1)
 CC SEQUENCE FROM N.A.
 CC MEDLINE=94067141; PubMed=8246995;
 CC Ivey-Hoyte M.C., Conroy R., Huber H.E., Goodhart P.J., Olfert A.,
 CC Heimbach D.C.,
 CC Cloning and characterization of E2F-2, a novel protein with the
 CC biochemical properties of transcription factor E2F-1.
 CC Mol. Cell. Biol. 13:7802-7812(1993).
 CC (2)
 CC SEQUENCE FROM N.A.
 CC Pearce A.,
 CC Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY
 CC WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE. TTCC/GCGC.
 CC FOUND IN THE PROMOTER REGION OF A NUMBER OF GENES WHOSE PRODUCTS
 CC ARE INVOLVED IN CELL CYCLE REGULATION OR IN DNA REPLICATION. THE
 CC DRP1/E2F COMPLEX FUNCTIONS IN THE CONTROL OF CELL-CYCLE
 CC PROGRESSION FROM G1 TO S PHASE. E2F-2 BINDS SPECIFICALLY TO RB1
 CC PROTEIN, IN A CELL-CYCLE DEPENDENT MANNER.
 CC -1- SUBUNIT: COMPONENT OF THE DRP1/E2F TRANSCRIPTION FACTOR COMPLEX.
 CC FORMS HETERODIMERS WITH DP FAMILY MEMBERS. THE E2F-2 COMPLEX BINDS
 CC SPECIFICALLY HYPOPHOSPHORYLATED RETINOBLASTOMA PROTEIN RB1. DURING
 CC THE CELL CYCLE, RB1 BECOMES PHOSPHORYLATED IN MID-TO-LATE G1
 CC PHASE, DETACHES FROM THE DRP1/E2F COMPLEX, RENDERING E2F
 CC TRANSCRIPTIONALLY ACTIVE. VIRAL ONCOPROTEINS, NOTABLY E1A, T-
 CC ANTIGEN AND HPV E7, ARE CAPABLE OF SEQUESTERING RB PROTEIN, THUS
 CC RELEASEING THE ACTIVE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVEL OF EXPRESSION IS FOUND IN
 CC PLACENTA, LOW LEVELS ARE FOUND IN LUNG. FOUND AS WELL IN MANY
 CC IMMORTALIZED CELL LINES DERIVED FROM TUMOR SAMPLES.
 CC -1- PTM: PHOSPHORYLATED BY CDK2 AND CYCLIN A-CDK2 IN THE S-PHASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
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 CC
 CC DR EMBL: L22846; AAA16890.1;
 CC DR EMBL: AL021154; CAA15949.1;
 CC DR HSSP: 016254; 1CF7.
 CC DR TRANSFAC: T01514;
 CC DR MIM: 600426;
 CC DR InterPro: IPR003316; E2F_TDP.
 CC DR Pfam: PF02319; E2F_TDP.1.
 CC DR Transcription regulation; Activator; DNA-binding; Nuclear protein;
 CC KW phosphorylation; Cell cycle.
 CC FT DOMAIN 65 105 CYCLIN A/CDK2 BINDING (POTENTIAL).
 CC FT DNM_BIND 107 196 POTENTIAL.
 CC FT DOMAIN 155 176 LEUCINE-ZIPPER.
 CC FT DOMAIN 160 196 DEF_BOX.
 CC FT DOMAIN 197 289 DIMERIZATION (POTENTIAL).
 CC FT DOMAIN 359 417 TRANSCRIPTION (POTENTIAL).
 CC FT DOMAIN 360 363 POLY-PRO.
 CC FT DOMAIN 410 427 RETINOBLASTOMA PROTEIN ASSOCIATION
 CC (POTENTIAL).
 CC FT SEQUENCE 437 AA; 47505 MW; 6054174233507205 CRC64;
 CC
 CC Query Match 37.4%; Score 69.5; DB 1; Length 437;
 CC Best Local Similarity 44.8%; Pred. No. 0.028;
 CC Matches 13; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

0Y 4 BRVYDALVYAMNISTK-KKEIRMG 31
 DB 166 KRRIIDVNLGSIOLIRKRNKNWVG 194
 RESULT 13
 E2F2_MOUSE STANDARD; PRT; 356 AA.
 ID E2F2_MOUSE
 AC 035261;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAR-2000 (Rel. 35, Last annotation update)
 DE Transcription factor E2F3 (E2F-3) (fragment).
 GN E2F3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC (1)
 CC SEQUENCE FROM N.A.
 CC STRAIN=SWISS ALBINO; TISSUE=fibroblast;
 CC MEDLINE=9802478; PubMed=9376316;
 CC Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L.,
 CC Phillips R.A.,
 CC Expression patterns of the E2F family of transcription factors
 CC during mouse neure system development.
 CC Mech. Dev. 66:13-25(1997).
 CC (2)
 CC DEVELOPMENTAL EXPRESSION.
 CC MEDLINE=87294022; PubMed=9149905;
 CC Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L.,
 CC Phillips R.A.,
 CC Expression patterns of the E2F family of transcription factors
 CC during murine epithelial development.
 CC Cell Growth Differ. 8:153-163(1997).
 CC -1- FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY
 CC WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE. TTCC/GCGC.
 CC FOUND IN THE PROMOTER REGION OF A NUMBER OF GENES WHOSE PRODUCTS
 CC ARE INVOLVED IN CELL CYCLE REGULATION OR IN DNA REPLICATION. THE
 CC DRP1/E2F COMPLEX FUNCTIONS IN THE CONTROL OF CELL-CYCLE
 CC PROGRESSION FROM G1 TO S PHASE. E2F-3 BINDS SPECIFICALLY TO RB1
 CC PROTEIN, IN A CELL-CYCLE DEPENDENT MANNER.
 CC -1- SUBUNIT: COMPONENT OF THE DRP1/E2F TRANSCRIPTION FACTOR COMPLEX.
 CC BINDS COOPERATIVELY WITH DP-1 TO E2F SITES. INTERACTS WITH
 CC RETINOBLASTOMA PROTEIN RB1 AND RELATED PROTEINS (SUCH AS P107)
 CC THAT INHIBIT THE E2F TRANSCRIPTION DOMAIN.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: IN THE DEVELOPING NERVOUS SYSTEM, HIGH LEVELS
 CC EXPRESSED IN BOTH VENTRAL AND DORSAL REGIONS OF THE SPINAL CORD
 CC FROM 13.5 DPC. ALSO EXPRESSED IN DORSAL ROOT AND CRANIAL GANGLIA
 CC IN 11.5-18.5 DPC EMBRYOS. ONLY LOW LEVELS OF EXPRESSION IN
 CC DEVELOPING BRAIN. IN THE DEVELOPING RETINA (13.5 DPC), EXPRESSION
 CC OF E2F-3 IS LOCALIZED TO THE GANGLION CELL LAYER. IN OTHER
 CC DEVELOPING TISSUES, EXPRESSED IN LIVER, LUNG AND HEART. SEAR
 CC EXPRESSION IN DEVELOPING KIDNEY AND SKELETAL MUSCLE. ABSENT FROM
 CC THE DEVELOPING CHOROID PLEXUS, THYMUS AND DEVELOPING SKIN. LOW
 CC LEVELS OF EXPRESSION IN THE DEVELOPING INTESTINAL EPITHELIUM AND
 CC MESENCHYME IN 12.5-18.5 DPC EMBRYOS.
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
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 CC
 CC DR EMBL: AF015948; AAB1671.1;
 CC DR HSSP: 016254; 1CF7.
 CC DR TRANSFAC: T02947;
 CC MCD; MGI:1096340; E2F3.

DR InterPro: IPR003316; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
 Cell cycle.
 FT NOVELTER 1 1
 FT DOMAIN 44 CYCLIN A/CDK2 BINDING (POTENTIAL).
 FT DNA_BIND 46 136 POTENTIAL.
 FT DOMAIN 95 116 LEUCINE-ZIPPER.
 FT DOMAIN 100 136 DBF BOX.
 FT DOMAIN 137 228 DIMERIZATION (POTENTIAL).
 FT DOMAIN 282 356 TRANSCRIPTION (POTENTIAL).
 FT DOMAIN 323 340 P130 PROTEIN ASSOCIATION (POTENTIAL).
 FT SEQUENCE 356 AA; 35007 MW; 078FCF4E0AC8E77 CRC64.

Query Match 36.8%; Score 68.5; DB 1; Length 356;
 Best Local Similarity 41.4%; Pred. No. 0.031;
 Matches 12; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

OY 4 RRAYDGLVLMAMWISKE-KKEIRNYG 31
 DB 106 KRRIIDTVNLESGIHLIKRSKNVQWNG 134

RESULT 14
 E2F3_HUMAN STANDARD; PRT; 465 AA.
 ID E2F3_HUMAN
 AC Q00716; 015000;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transcription factor E2F3 (E2F-3).
 GN E2F3 OR KIA00075.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94067143; PubMed-8246996;
 RA Lees J.A., Saito M., Vidal M., Valentine M., Look T., Harlow E.,
 RA Dyson N., Hellm K.;
 RT "The retinoblastoma protein binds to a family of E2F transcription
 RT factors.";
 RT Mol. Cell. Biol. 13:7813-7825(1993).
 RN [2]
 RP SEQUENCE OF 292-465 FROM N.A.
 RC TISSUE-Bone marrow;
 RM MEDLINE-96051198; PubMed-7584044;
 RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
 RA Beil N., Kawarabayashi Y., Ishikawa K.-I., Tadate S.;
 RT "Prediction of the coding sequences of unidentified human genes. II.
 RT The coding sequences of 40 new genes (KIA004-KIA0080) deduced by
 RT analysis of cDNA clones from human cell line KG-1.";
 RT DNA Res. 1:223-229(1994).
 RN [3]
 RP FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY
 WITH DP PROTEIN THROUGH THE E2 RECOGNITION SITE, TTCC/GCC,
 FOUND IN THE PROMOTER REGION OF A NUMBER OF GENES WHOSE PRODUCTS
 ARE INVOLVED IN CELL CYCLE REGULATION OR IN DNA REPLICATION. THE
 DBP/E2F COMPLEX FUNCTIONS IN THE CONTROL OF CELL-CYCLE
 PROGRESSION FROM G1 TO S PHASE. E2F-3 BINDS SPECIFICALLY TO RB1
 PROTEIN, IN A CELL-CYCLE DEPENDENT MANNER.
 CC SUBUNIT: COMPONENT OF THE DBP1/E2F TRANSCRIPTION FACTOR COMPLEX.
 CC BINDS COOPERATIVELY WITH DP-1 TO E2F SITES. INTERACTS WITH
 CC RETINOBLASTOMA PROTEIN RB1 AND RELATED PROTEINS (SUCH AS P107)
 CC THAT INHIBIT THE E2F TRANSCRIPTIONAL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Nucleus.
 CC -1- SIMILARITY: BELONGS TO THE E2F/DP FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

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 CC entities requires a license agreement (see <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).

DR EMBL: Y10479; CAAT7504.1;
 DR EMBL: D38550; BAA07553.1;
 DR HSPG: 016284; 1CF7.
 DR KIM: 600427;
 DR InterPro: IPR003316; E2F_TDP.
 DR Pfam: PF02319; E2F_TDP; 1.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
 Cell cycle.

FT NOVELTER 26 31
 FT DOMAIN 45 53 POLY-ALA.
 FT DOMAIN 101 153 CYCLIN A/CDK2 BINDING (POTENTIAL).
 FT DOMAIN 120 129 POLY-GLY.
 FT DNA_BIND 355 245 POTENTIAL.
 FT DOMAIN 204 225 LEUCINE-ZIPPER.
 FT DOMAIN 209 245 DBF BOX.
 FT DOMAIN 246 337 DIMERIZATION (POTENTIAL).
 FT DOMAIN 391 465 TRANSCRIPTION (POTENTIAL).
 FT DOMAIN 432 449 RETINOBLASTOMA PROTEIN ASSOCIATION
 (POTENTIAL).
 FT SEQUENCE 465 AA; 49161 MW; 4611565842CA99EC CRC64;

Query Match 36.8%; Score 68.5; DB 1; Length 465;
 Best Local Similarity 41.4%; Pred. No. 0.041;
 Matches 12; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

OY 4 RRAYDGLVLMAMWISKE-KKEIRNYG 31
 DB 215 KRRIIDTVNLESGIHLIKRSKNVQWNG 243

RESULT 15
 E2F_DROME STANDARD; PRT; 805 AA.
 ID E2F_DROME
 AC Q27368; 077035;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Transcription factor E2f (de2f).
 GN E2F OR E2F1 OR CG6376.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
 OC Euryptera; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-Eye imaginal disk;
 RC MEDLINE-94294381; PubMed-8027287;
 RA Driulich B.D., Brock A., Dambolt M., Yenush L., Dyson N.;
 RT "DNA-binding and trans-activation properties of Drosophila E2F and DP
 RT proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:6359-6363(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RM MEDLINE-94158833; PubMed-8114698;
 RA Ohtani N., Nevins J.R.;
 RT "Functional properties of a Drosophila homolog of the E2F1 gene.";
 RT Mol. Cell. Biol. 14:1603-1612(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RM STRAIN-ORSON-R;
 RA MEDLINE-99072992; PubMed-9858578;
 RA Sasaki T., Sawada T., Yamaguchi M., Shimomiyu T.;
 RT "Specification of regions of DNA replication initiation during
 RT embryogenesis in the 65-kilobase DNA replication-d2f locus of Drosophila
 RT melanogaster.";
 RT Mol. Cell. Biol. 19:547-555(1999).
 RN [4]

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Page 12

Wed Aug 28 13:32:29 2002

US-09-900-147-1.ral

Page 1

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: August 28, 2002, 12:57:09 ; Search time 12.99 seconds
(without alignments)
69.573 Million cell updates/sec

Title: US-09-900-147-1

Perfect score: 186
Sequence: 1 KNIRRYDALNTLVAMNISKERKIKGLPTNSA 37

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: Issued Patents, AA: *
2: /cgn2.6/pdata/2/laa/3A.COMB.pep: *
3: /cgn2.6/pdata/2/laa/5B.COMB.pep: *
4: /cgn2.6/pdata/2/laa/6A.COMB.pep: *
5: /cgn2.6/pdata/2/laa/6B.COMB.pep: *
6: /cgn2.6/pdata/2/laa/6C.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	37	4 US-09-308-935-1	Sequence 1, Appl 1
2	186	100.0	72	2 US-08-428-131-11	Sequence 11, Appl 1
3	186	100.0	72	4 US-09-078-596-11	Sequence 11, Appl 1
4	186	100.0	410	2 US-08-723-415B-10	Sequence 10, Appl 1
5	186	100.0	410	2 US-08-723-415B-11	Sequence 11, Appl 1
6	186	100.0	410	2 US-08-428-131-2	Sequence 2, Appl 1
7	186	100.0	410	2 US-08-602-846-2	Sequence 2, Appl 1
8	186	100.0	410	4 US-09-078-596-2	Sequence 2, Appl 1
9	186	100.0	410	4 US-09-189-627A-10	Sequence 10, Appl 1
10	186	100.0	410	4 US-08-189-627A-11	Sequence 11, Appl 1
11	186	97.8	369	2 US-08-723-415B-4	Sequence 4, Appl 1
12	186	97.8	369	2 US-08-189-627A-4	Sequence 4, Appl 1
13	186	97.8	370	2 US-08-723-415B-6	Sequence 6, Appl 1
14	186	97.8	370	2 US-08-189-627A-6	Sequence 6, Appl 1
15	186	97.8	385	2 US-08-723-415B-8	Sequence 8, Appl 1
16	186	97.8	385	2 US-09-189-627A-8	Sequence 8, Appl 1
17	186	97.8	446	2 US-08-723-415B-2	Sequence 2, Appl 1
18	186	97.8	446	2 US-09-189-627A-2	Sequence 2, Appl 1
19	186	97.8	446	2 US-09-308-935-6	Sequence 6, Appl 1
20	186	97.8	446	2 US-09-308-935-4	Sequence 4, Appl 1
21	186	97.8	446	2 US-09-308-935-3	Sequence 3, Appl 1
22	186	97.8	446	2 US-09-308-935-1	Sequence 1, Appl 1
23	186	97.8	446	2 US-09-308-935-11	Sequence 11, Appl 1
24	186	97.8	446	2 US-09-308-935-10	Sequence 10, Appl 1
25	186	97.8	446	2 US-09-308-935-17	Sequence 17, Appl 1
26	186	97.8	446	2 US-09-308-935-16	Sequence 16, Appl 1
27	186	97.8	446	2 US-09-308-935-15	Sequence 15, Appl 1

28	76	40.9	16	4 US-09-308-935-5	Sequence 5, Appl 1
29	71.5	38.4	73	2 US-08-428-131-12	Sequence 12, Appl 1
30	71.5	38.4	73	4 US-09-078-596-12	Sequence 12, Appl 1
31	71.5	38.4	196	2 US-08-481-814A-9	Sequence 9, Appl 1
32	71.5	38.4	437	1 US-08-136-119-4	Sequence 4, Appl 1
33	71.5	38.4	437	1 US-07-682-711-2	Sequence 2, Appl 1
34	71.5	38.4	437	2 US-08-723-415B-13	Sequence 13, Appl 1
35	71.5	38.4	437	2 US-08-481-814A-6	Sequence 6, Appl 1
36	71.5	38.4	437	2 US-08-462-174-2	Sequence 2, Appl 1
37	71.5	38.4	437	3 US-08-801-093-1	Sequence 1, Appl 1
38	71.5	38.4	437	4 US-09-189-627A-13	Sequence 13, Appl 1
39	71.5	38.4	476	2 US-08-139-937-14	Sequence 14, Appl 1
40	71.5	38.4	476	2 PCT-0593-11310-14	Sequence 14, Appl 1
41	69.5	37.4	437	1 US-08-136-119-2	Sequence 2, Appl 1
42	69.5	37.4	437	2 US-08-481-814A-7	Sequence 7, Appl 1
43	69.5	37.1	14	4 US-09-308-935-11	Sequence 11, Appl 1
44	65.5	35.2	413	2 US-08-481-814A-8	Sequence 8, Appl 1
45	65.5	35.2	413	3 US-08-836-582-2	Sequence 2, Appl 1

ALIGNMENTS

Surgeal steel

RESULT 1
US-09-308-935-1
Sequence 1, Application US/09308935
Patent No. 6268334
GENERAL INFORMATION:
APPLICANT: Bandara, Nicholas B
APPLICANT: Le Thanh, Nicholas B
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9626569.7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1
LENGTH: 37
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-1
Query Match 100.0%; Score 186; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 KNIRRYDALNTLVAMNISKERKIKGLPTNSA 37
1 KNIRRYDALNTLVAMNISKERKIKGLPTNSA 37
RESULT 2 *claims DNA*
US-08-428-131-11
Sequence 11, Application US/08428131
Patent No. 5863157
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Nixon & Vandierhe
STREET: 1100 No. 586375th Glebe Road, 8th floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-131-11

Query Match 100.0% Score 186; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 KNIRRYDALVLAAMNISKKEIKIGLPTNSA 37
|||||
DB 4 KNIRRYDALVLAAMNISKKEIKIGLPTNSA 40

sub body

US-09-078-596-11
Sequence 11, Application US/09078536
Patent No. 6150116
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderrhye
STREET: 1100 No. 6150116th Glebe Road, 8th floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-078-596-11

Query Match 100.0% Score 186; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 KNIRRYDALVLAAMNISKKEIKIGLPTNSA 37
|||||
DB 4 KNIRRYDALVLAAMNISKKEIKIGLPTNSA 40

US-08-723-415B-10
Sequence 10, Application US/08723415B
Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: Lathangue, Nicholas B.
TITLE OF INVENTION: Transcription Factor DP-3 AND ISOFORMS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERRHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 415
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-10

Query Match 100.0% Score 186; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 KNIRRYDALVLAAMNISKKEIKIGLPTNSA 37
|||||
DB 163 KNIRRYDALVLAAMNISKKEIKIGLPTNSA 199

US-08-723-415B-11
Sequence 11, Application US/08723415B

Wed Aug 28 13:32:29 2002

us-09-900-147-1.ral

Page 3

Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: LATHAQUE, Nicholas B.
APPLICANT: delaluna, Susan
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NO. 5859199th Globe Rd. 8th floor
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-11

Query Match 100.0%; Score 186; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

01 1 KNIRRVYDALVLMANNISKEKKEIKIGLPTNSA 37
DB 163 KNIRRVYDALVLMANNISKEKKEIKIGLPTNSA 196

RESULT 6
US-08-428-131-2
Sequence 2, Application US/08428131
Patent No. 5863757
GENERAL INFORMATION:
APPLICANT: LA THANHUE, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE
STREET: 1100 NO. 5863757th Globe Road, 8th floor
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-131-2

Query Match 100.0%; Score 186; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

01 1 KNIRRVYDALVLMANNISKEKKEIKIGLPTNSA 37
DB 163 KNIRRVYDALVLMANNISKEKKEIKIGLPTNSA 199

RESULT 7
US-08-602-846-2
Sequence 2, Application US/08602846
Patent No. 5871901
GENERAL INFORMATION:
APPLICANT: LA THANHUE, Nicholas B.
TITLE OF INVENTION: ASSAY FOR INHIBITORS OF DP-1 AND OTHER DP
TITLE OF INVENTION: PROTEINS.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 8th floor, 1100 NO. 5871901th Globe Road
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,846
FILING DATE: 26-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 620-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-602-846-2

Query Match 100.0%; Score 186; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Aug 28 13:32:29 2002

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Page 4

QY 1 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 37
DB 163 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 199

US-09-078-596-2
Sequence 2, Application US/09078596

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrye
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderye
STREET: 1100 No. 6150116th Glebe Road, 8th floor
CITY: Arlington
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ALBERT R. CRAWFORD
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-078-596-2

Query Match 100.0%; Score 186; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 37
DB 163 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 199

US-09-189-627A-10
Sequence 10, Application US/09189627A

GENERAL INFORMATION:
APPLICANT: de la Lanza, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 10
LENGTH: 410
TYPE: PRT
ORGANISM: human
US-09-189-627A-10

Query Match 100.0%; Score 186; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 37
DB 163 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 199

US-09-189-627A-11
Sequence 11, Application US/09189627A

GENERAL INFORMATION:
APPLICANT: de la Lanza, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 11
LENGTH: 410
TYPE: PRT
ORGANISM: mouse
US-09-189-627A-11

Query Match 100.0%; Score 186; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 37
DB 163 KNIRRYDALNVMNNISKEKEIKWGLPTNSA 199

US-08-723-415B-2
Sequence 4, Application US/08723415B

GENERAL INFORMATION:
APPLICANT: de la Lanza, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERYE P.C.
STREET: 1100 No. 585199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

Wed Aug 28 13:32:29 2002

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Page 5

APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-4

Query Match 97.8% Score 182; DB 2; Length 369;
Best Local Similarity 97.3% Pred. No. 8,4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 101 ENIRRYDALVLMANNISKEKEIKWIGLPTNSA 137

RESULT 12
US-09-189-627A-4
Sequence 4, Application US/09189627A
Patent No. 6159691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 4
LENGTH: 369
TYPE: PRT
ORGANISM: mouse
US-09-189-627A-4

Query Match 97.8% Score 182; DB 4; Length 369;
Best Local Similarity 97.3% Pred. No. 8,4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 101 ENIRRYDALVLMANNISKEKEIKWIGLPTNSA 137

RESULT 13
US-08-723-415B-6
Sequence 6, Application US/08723415B
Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: Lathangue, Nicholas B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NO. 5859199th Giebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 01.0, Version 01.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-6

Query Match 97.8% Score 182; DB 2; Length 370;
Best Local Similarity 97.3% Pred. No. 8,4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 102 ENIRRYDALVLMANNISKEKEIKWIGLPTNSA 138

RESULT 14
US-09-189-627A-6
Sequence 6, Application US/09189627A
Patent No. 6159691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 6
LENGTH: 370
TYPE: PRT
ORGANISM: mouse
US-09-189-627A-6

Query Match 97.8% Score 182; DB 4; Length 370;
Best Local Similarity 97.3% Pred. No. 8,4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Page 6

07 1 KNIRRYDANVAMNIIISKEKRNIGLPTNSA 37
DB 102 ENIRRYDANVAMNIIISKEKRNIGLPTNSA 138

RESULT 15
US-08-723-4158-8

Sequence 8, Application US/087234158
Patent No. 5859199

GENERAL INFORMATION:

APPLICANT: LATHROUE, Nicholas B.

APPLICANT: delaluna, Susana

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOPRONS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NO. 5859199th Globe Rd. 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIA TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723,415B

FILING DATE: 30-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9610195.1

FILING DATE: 15-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R.

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 385 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-723-4158-8

102 e

Query Match 97.8% Score 182, DB 2, Length 385;
Best Local Similarity 97.3% Pred. No. 8, 8e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
07 1 KNIRRYDANVAMNIIISKEKRNIGLPTNSA 37
DB 117 ENIRRYDANVAMNIIISKEKRNIGLPTNSA 153

Search completed: August 28, 2002, 13:59:33
Job time: 144 sec

Wed Aug 28 13:32:29 2002

us-09-900-147-1.ral

Page 1

GenCore version 4.5
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OM protein - protein search, using sv model

Run on: August 28, 2002, 12:57:09 ; Search time 12.99 Seconds
(without alignments)
69.573 Million cell updates/sec

Title: US-09-900-147-1

Sequence: 1 KNIRRYTDLVLMANNISKEKEIKWIGLPTNSA 37

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summariesDatabase: Issued_Patents_AA:
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:
5: /cgn2_6/ptodata/2/1aa/PTCUTS.COMB.pep:
6: /cgn2_6/ptodata/2/1aa/Backfillal.pep:Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	186	100.0	37	4	US-09-308-935-1
2	186	100.0	72	2	US-08-428-131-11
3	186	100.0	72	4	US-09-078-596-11
4	186	100.0	410	2	US-08-723-415B-13
5	186	100.0	410	2	US-08-723-415B-11
6	186	100.0	410	2	US-08-428-131-2
7	186	100.0	410	2	US-08-602-846-2
8	186	100.0	410	4	US-09-078-596-2
9	186	100.0	410	4	US-09-189-627A-10
10	186	100.0	410	4	US-09-189-627A-11
11	186	97.8	369	2	US-08-723-415B-4
12	182	97.8	370	2	US-08-723-415B-6
13	182	97.8	370	4	US-09-189-627A-6
14	182	97.8	385	2	US-08-723-415B-8
15	182	97.8	385	4	US-09-189-627A-8
16	182	97.8	446	2	US-08-723-415B-2
17	182	97.8	446	4	US-09-189-627A-2
18	182	97.8	446	4	US-09-308-935-6
19	182	97.8	446	4	US-09-308-935-4
20	182	97.8	446	4	US-09-308-935-3
21	182	97.8	446	4	US-09-308-935-1
22	182	97.8	446	4	US-09-308-935-13
23	182	97.8	446	4	US-08-428-131-13
24	182	97.8	446	4	US-09-078-596-13
25	182	97.8	446	4	US-09-308-935-10
26	182	97.8	446	4	US-09-308-935-17
27	182	97.8	446	4	US-09-308-935-16

28	76	40.9	16	4	US-09-308-935-5	Sequence 5, Appl
29	71.5	38.4	73	2	US-08-428-131-12	Sequence 12, Appl
30	71.5	38.4	73	4	US-09-078-596-12	Sequence 12, Appl
31	71.5	38.4	196	2	US-08-481-814A-9	Sequence 9, Appl
32	71.5	38.4	437	1	US-08-136-119-4	Sequence 4, Appl
33	71.5	38.4	437	1	US-07-882-711-2	Sequence 2, Appl
34	71.5	38.4	437	2	US-08-723-415B-13	Sequence 13, Appl
35	71.5	38.4	437	2	US-08-481-814A-6	Sequence 6, Appl
36	71.5	38.4	437	2	US-08-462-174-2	Sequence 2, Appl
37	71.5	38.4	437	2	US-08-601-092-1	Sequence 1, Appl
38	71.5	38.4	437	4	US-08-189-627A-13	Sequence 13, Appl
39	71.5	38.4	476	2	US-08-139-937-14	Sequence 14, Appl
40	71.5	38.4	476	5	PCT-US93-11310-14	Sequence 14, Appl
41	69.5	37.4	437	1	US-08-136-119-2	Sequence 2, Appl
42	69.5	37.4	437	2	US-08-481-814A-7	Sequence 7, Appl
43	69	37.1	14	4	US-09-308-935-11	Sequence 11, Appl
44	65.5	35.2	413	2	US-08-481-814A-8	Sequence 8, Appl
45	65.5	35.2	413	2	US-08-836-582-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-308-935-1
Sequence 1, Application US/09308935
Patent No. 6268334

SUNY at State

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT FILING DATE: 1999-05-27
EARLIER FILING DATE: 1997-12-23
PCT/CB97/03506
EARLIER APPLICATION NUMBER: GS 9626589.7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1SEQ ID NO 1
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-1Query Match 100.0%; Score 186; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;CY 1 KNIRRYTDLVLMANNISKEKEIKWIGLPTNSA 37
DB 1 KNIRRYTDLVLMANNISKEKEIKWIGLPTNSA 37RESULT 2
US-08-428-131-11
Sequence 11, Application US/08428131
Patent No. 5863757GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Niton & Vandaele
STREET: 1100 No. 5863757th Glebe Road, 8th floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
08-428-131-11

Query Match 100.0% Score 186; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 KNIRRYDALNVLMNNISKEKKEINIGLPTNSA 37
4 KNIRRYDALNVLMNNISKEKKEINIGLPTNSA 40

RESULT 3 *but it had*
US-09-078-596-11

Sequence 11, Application US/09078536

Patent No. 6150116

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas Barrie

TITLE OF INVENTION: Transcription Factor DP-1

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSER: Nixon & Vandehyve

STREET: 1100 No. 6150116th Glebe Road, 8th floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/078,596

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/428,131

FILING DATE: 23-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Arthur R. Crawford

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-181

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4100

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids

TYPE: amino acid

STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-078-596-11

Query Match 100.0% Score 186; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 KNIRRYDALNVLMNNISKEKKEINIGLPTNSA 37
4 KNIRRYDALNVLMNNISKEKKEINIGLPTNSA 40

RESULT 4
US-08-723-4158-10

Sequence 10, Application US/087234158

Patent No. 5859199

GENERAL INFORMATION:

APPLICANT: LaThangue, Nicholas B.

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS

THEREOF

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSER: NIXON & VANDERHYE P.C.

STREET: 1100 No. 5859199th Glebe Rd, 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723,4158

FILING DATE: 30-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9610195.1

FILING DATE: 15-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R.

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 410 amino acids

TYPE: amino acid

STRANDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-723-4158-10

Query Match 100.0% Score 186; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 KNIRRYDALNVLMNNISKEKKEINIGLPTNSA 37
163 KNIRRYDALNVLMNNISKEKKEINIGLPTNSA 199

RESULT 5

US-08-723-4158-11

Sequence 11, Application US/087234158

Patent No. 5839199
 GENERAL INFORMATION:
 APPLICANT: LaThangue, Nicholas B.
 APPLICANT: delatuna, Susana
 TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 No. 5859199th Glebe Rd. 8th floor
 CITY: Arlington
 STATE: VA USA
 COUNTRY: USA
 ZIP: 22201-4741
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/723,415B
 FILING DATE: 30-SEP-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9610195.1
 FILING DATE: 15-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Crawford, Arthur R.
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 117-220
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-816-4000
 TELEFAX: 703-816-4100
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-723-415B-11

Query Match 100.0% Score 186; DB 2; Length 410;
 Best Local Similarity 100.0%; Pred. No. 2,3e-20;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KNIRRYDALTVMNNIISKKEIKNIQLPNTSA 37
 DB 163 KNIRRYDALTVMNNIISKKEIKNIQLPNTSA 159

RESULT 6
 US-08-428-131-2
 Sequence 2, Application US/08428131
 Patent No. 5863257
 GENERAL INFORMATION:
 APPLICANT: LaThangue, Nicholas BATTLE
 TITLE OF INVENTION: Transcription Factor DP-1
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye
 STREET: 1100 No. 5863257th Glebe Road, 8th floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.23 (EPO)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/428,131
 FILING DATE: 23-JUN-1995
 CLASSIFICATION: 516
 ATTORNEY/AGENT INFORMATION:
 NAME: Arthur R. Crawford
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 117-181
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-428-131-2

Query Match 100.0% Score 186; DB 2; Length 410;
 Best Local Similarity 100.0%; Pred. No. 2,3e-20;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KNIRRYDALTVMNNIISKKEIKNIQLPNTSA 37
 DB 163 KNIRRYDALTVMNNIISKKEIKNIQLPNTSA 199

RESULT 7
 US-08-602-846-2
 Sequence 2, Application US/08602846
 Patent No. 5871501
 GENERAL INFORMATION:
 APPLICANT: LaThangue, Nicholas B
 TITLE OF INVENTION: ASSAY FOR INHIBITORS OF DP-1 AND OTHER DP
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye PC
 STREET: 8th floor, 1100 No. 5871501th Glebe Road
 CITY: Arlington
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,846
 FILING DATE: 26-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Crawford, Arthur R.
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 620-12
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-602-846-2

Query Match 100.0% Score 186; DB 2; Length 410;
 Best Local Similarity 100.0%; Pred. No. 2,3e-20;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Page 4

QY 1 KNIRRYDALVAMNISKKEIKNIGLPTNSA 37
DB 163 KNIRRYDALVAMNISKKEIKNIGLPTNSA 199

RESULT 8

US-09-078-596-2
Sequence 2, Application US/09078596

PATENT NO. 6150116
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS BARRIE
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE
STREET: 1100 NO. 6150116TH GLEBE ROAD, 8th FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ARTHUR R. GRAVITORD
REGISTRATION NUMBER: 25,317
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-078-596-2

Query Match 100.0%; Score 186; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRYDALVAMNISKKEIKNIGLPTNSA 37
DB 163 KNIRRYDALVAMNISKKEIKNIGLPTNSA 199

RESULT 9

US-09-189-627A-10
Sequence 10, Application US/09189627A

PATENT NO. 6159691
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 10
LENGTH: 410
TYPE: PRT
ORGANISM: human
US-09-189-627A-10

Query Match 100.0%; Score 186; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRYDALVAMNISKKEIKNIGLPTNSA 37
DB 163 KNIRRYDALVAMNISKKEIKNIGLPTNSA 199

RESULT 10

US-09-189-627A-11
Sequence 11, Application US/09189627A

PATENT NO. 6159691
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 11
LENGTH: 410
TYPE: PRT
ORGANISM: mouse
US-09-189-627A-11

Query Match 100.0%; Score 186; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 2,3e-20;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNIRRYDALVAMNISKKEIKNIGLPTNSA 37
DB 163 KNIRRYDALVAMNISKKEIKNIGLPTNSA 199

RESULT 11

US-08-723-415B
Sequence 4, Application US/08723415B

PATENT NO. 5851919
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NO. 5851919TH GLEBE RD. 8th FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-4

Query Match 97.8% Score 182; DB 2; Length 369;
Best Local Similarity 97.3% Pred. No. 8.4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 101 ENIRRYDALVLMNMNIISEKKEIKWIGLPTNSA 37
:|||||

RESULT 12
US-09-189-627A-4
Sequence 4, Application US/09189627A
Patent No. 6139691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
PRIOR FILING DATE: 1996-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 369
TYPE: PRT
ORGANISM: mouse
US-09-189-627A-4

Query Match 97.8% Score 182; DB 4; Length 369;
Best Local Similarity 97.3% Pred. No. 8.4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 101 ENIRRYDALVLMNMNIISEKKEIKWIGLPTNSA 37
:|||||

RESULT 13
US-08-723-415B-6
Sequence 6, Application US/08723415B
Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: delaluna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
THEREOF

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERBYE P.C.
STREET: 1100 NO. 3859195th globe rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.0, Version 91.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-6

Query Match 97.8% Score 182; DB 2; Length 370;
Best Local Similarity 97.3% Pred. No. 8.4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 102 ENIRRYDALVLMNMNIISEKKEIKWIGLPTNSA 138
:|||||

RESULT 14
US-09-189-627A-6
Sequence 6, Application US/09189627A
Patent No. 6139691
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
PRIOR FILING DATE: 1996-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 370
TYPE: PRT
ORGANISM: mouse
US-09-189-627A-6

Query Match 97.8% Score 182; DB 4; Length 370;
Best Local Similarity 97.3% Pred. No. 8.4e-20;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KNIRRYDALNVLMMNIIISKEKEIKWICLPTNSA 37
DB 102 ENIRRYDALNVLMMNIIISKEKEIKWICLPTNSA 138

RESULT 15
US-08-723-4158-8

Sequence 8. Application US/087234158
Patent No. 5859199

GENERAL INFORMATION:

APPLICANT: Lazarene, Nicholas B.

TITLE OF INVENTION: delatuna, susana

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 No. 5859199th Glebe Rd.

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723-4158

FILING DATE: 30-SEP-1996

CLASSIFICATION: A35

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9610195.1

FILING DATE: 13-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R.

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4100

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 385 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-723-4158-8

102 e

Query Match 97.8% Score 182; DB 2; Length 385;
eat Local Similarity 97.3% Pred. No. 8.8e-20;
atches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNIRRYDALNVLMMNIIISKEKEIKWICLPTNSA 37
DB 117 ENIRRYDALNVLMMNIIISKEKEIKWICLPTNSA 153

Search completed: August 28, 2002, 12:59:33
Job time: 144 sec